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(71)	*Sökande* *Applicant (s)*	*Forskarpatent i Syd AB, Lund SE*
(21)	*Patentansökningsnummer* *Patent application number*	*0302312-4*
(86)	*Ingivningsdatum* *Date of filing*	*2003-08-27*
(30)	*Prioritet begärd från*	*2002-10-04 SE 0202959-3*

Stockholm, 2006-10-25

För Patent- och registreringsverket
For the Patent- and Registration Office

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Avgift
Fee 170:-

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TITLE

PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR TREATMENT OF ATHEROSCLEROSIS

DESCRIPTION

Technical field

The present invention relates to new recombinant human antibodies raised against peptides being derivatives of apolipoprotein B, in particular antibodies to be used for immunization therapy for treatment of atherosclerosis, method for their preparation, and method for passive immunization using said antibodies.

In particular the invention includes:

The use of any isolated recombinant antibody raised against an oxidized form of the peptides listed in table 1, in particular MDA-modified peptides, preferably together with a suitable carrier and adjuvant as an immunotherapy or "anti-atherosclerosis "vaccine" for prevention and treatment of ischemic cardiovascular disease.

Background of the invention

The protective effects of humoral immunity are known to be mediated by a family of structurally related glycoproteins called antibodies. Antibodies initiate their biological activity by binding to antigens. Antibody binding to antigens is generally specific for one antigen and the binding is usually of high affinity. Antibodies are produced by B-lymphocytes. Blood contains many different antibodies, each derived from a clone of B-cells and each having a distinct structure and specificity for antigen. Antibodies are present on the surface of B-lymphocytes, in the plasma, in interstitial fluid of the tissues and in secretory fluids such as saliva and mucous on mucosal surfaces.

All antibodies are similar in their overall structure, accounting for certain similarities in physico-chemical features such as charge and solubility. All antibodies have a common core structure of two identical light chains, each about 24 kilodaltons, and two identical heavy chains of about 55-70 kilodaltons each. One light chain is attached to each heavy chain, and the two heavy chains are attached to each other. Both the light and heavy chains contain a series of repeating homologous units, each of about 110 amino acid residues in length which fold independently in a common globular motif, called an immunoglobulin (Ig) domain. The region of an antibody formed by the association of the two heavy chains is hydrophobic. Antibodies, and especially monoclonal antibodies, are known to cleave at the site where the light chain attaches to the heavy chain when they are subjected to adverse physical or chemical conditions. Because antibodies contain numerous cysteine residues, they have many cysteine-cysteine disulfide bonds. All Ig domains contain two layers of beta-pleated sheets with three or four strands of anti-parallel polypeptide chains.

Despite their overall similarity, antibody molecules can be divided into a small number of distinct classes and subclasses based on physicochemical characteristics such as size, charge and solubility, and on their behavior in binding to antigens. In humans, the classes of antibody molecules are: IgA, IgD, IgE, IgG and IgM. Members of each class are said to be of the same isotype. IgA and IgG isotypes are further subdivided into subtypes called IgA1, IgA2 and IgG1, IgG2, IgG3 and IgG4. The heavy chains of all antibodies in an isotype share extensive regions of amino acid sequence identity, but differ from antibodies belonging to other isotypes or subtypes. Heavy chains are designated by the letters of the Greek alphabet corresponding to the overall isotype of the antibody, e.g., IgA contains .alpha., IgD contains .delta., IgE contains .epsilon., IgG contains .gamma., and IgM contains .mu. heavy chains. IgG, IgE and IgD circulate as monomers, whereas secreted forms of IgA and IgM are dimers or pentamers, respectively, stabilized by the J chain. Some IgA molecules exist as monomers or trimers.

There are between 10^8 and 10^{10} structurally different antibody molecules in every individual, each with a unique amino acid sequence in their antigen combining sites. Sequence diversity in antibodies is predominantly found in three short stretches within the amino terminal domains of the heavy and light chains called variable (V) regions, to distinguish them from the more conserved constant (C) regions.

Atherosclerosis is a chronic disease that causes a thickening of the innermost layer (the intima) of large and medium-sized arteries. It decreases blood flow and may cause ischemia and tissue destruction in organs supplied by the affected vessel. Atherosclerosis is the major cause of cardiovascular disease including myocardial infarction, stroke and peripheral artery disease. It is the major cause of death in the western world and is predicted to become the leading cause of death in the entire world within two decades.

The disease is initiated by accumulation of lipoproteins, primarily low-density lipoprotein (LDL), in the extracellular matrix of the vessel. These LDL particles aggregate and undergo oxidative modification. Oxidized LDL is toxic and cause vascular injury.

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Atherosclerosis represents in many respects a response to this injury including inflammation and fibrosis.

In 1989 Palinski and coworkers identified circulating autoantibodies against oxidized LDL in humans. This observation suggested that atherosclerosis may be an autoimmune disease caused by immune reactions against oxidized lipoproteins. At this time several laboratories began searching for associations between antibody titers against oxidized LDL and cardiovascular disease. However, the picture that emerged from these studies was far from clear. Antibodies existed against a large number of different epitopes in oxidized LDL, but the structure of these epitopes was unknown. The term "oxidized LDL antibodies" thus referred to an unknown mixture of different antibodies rather than to one specific antibody. T cell-independent IgM antibodies were more frequent than T-cell dependent IgG antibodies.

Antibodies against oxidized LDL were present in both patients with cardiovascular disease and in healthy controls. Although some early studies reported associations between oxidized LDL antibody titers and cardiovascular disease, others were unable to find such associations. A major weakness of these studies was that the ELISA tests used to determine antibody titers used oxidized LDL particles as ligand. LDL composition is different in different individuals, the degree of oxidative modification is difficult both to control and assess and levels of antibodies against the different epitopes in the oxidized LDL particles can not be determined. To some extent, due to the technical problems it has been difficult to evaluate the role of antibody responses against oxidized LDL using the techniques available so far, but, however, it is not possible to create well defined and reproducable components of a vaccine if one should use intact oxidized LDL particles.

Another way to investigate the possibility that autoimmune reactions against oxidized LDL in the vascular wall play a key role in the development of atherosclerosis is to immunize animals against its own oxidized LDL. The idea behind this approach is that if autoimmune reactions against oxidized LDL are reinforced using classical immunization techniques this would result in increased vascular inflammation and progressive of atherosclerosis. To test this hypothesis rabbits were immunized with homologous oxidized LDL and then induced atherosclerosis by feeding the animals a high-cholesterol diet for 3 months.

However, in contrast to the original hypothesis immunization with oxidized LDL had a protective effect reducing atherosclerosis with about 50%. Similar results were also obtained in a subsequent study in which the high-cholesterol diet was combined with vascular balloon-injury to produce a more aggressive plaque development. In parallel with our studies several other laboratories reported similar observations. Taken together the available data clearly demonstrates that there exist immune reactions that protect against the development of atherosclerosis and that these involves autoimmunity against oxidized LDL.

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These observations also suggest the possibility of developing an immune therapy or "vaccine" for treatment of atherosclerosis-based cardiovascular disease in man. One approach to do this would be to immunize an individual with his own LDL after it has been oxidized by exposure to for example copper. However, this approach is complicated by the fact that it is not known which structure in oxidized LDL that is responsible for inducing the protective immunity and if oxidized LDL also may contain epitopes that may give rise to adverse immune reactions.

The identification of epitopes in oxidized LDL is important for several aspects:

First, one or several of these epitopes are likely to be responsible for activating the anti-atherogenic immune response observed in animals immunized with oxidized LDL. Peptides containing these epitopes may therefore represent a possibility for development of an immune therapy or "atherosclerosis vaccine" in man. Further, they can be used for therapeutic treatment of atheroschlerosis developed in man.

Secondly, peptides containing the identified epitopes can be used to develop ELISAs able to detect antibodies against specific structure in oxidized LDL. Such ELISAs would be more precise and reliable than ones presently available using oxidized LDL particles as antigen. It would also allow the analyses of immune responses against different epitopes in oxidized LDL associated with cardiovascular disease.

US patent 5,972,890 relates to a use of peptides for diagnosing atherosclerosis. The technique presented in said US patent is as a principle a form of radiophysical diagnosis. A peptide sequence is radioactively labelled and is injected into the bloodstream. If this peptide sequence should be identical with sequences present in apolipoprotein B it will bind to the tissue where there are receptors present for apolipoprotein B. In vessels this is above all atherosclerotic plaque. The concentration of radioactivity in the wall of the vessel can then be determined e.g., by means of a gamma camera. The technique is thus a radiophysical diagnostic method based on that radioactively labelled peptide sequences will bound to their normal tissue receptors present in atherosclerotic plaque and are detected using an external radioactivity analysis. It is a direct analysis method to identify atherosclerotic plaque. It requires that the patient be given radioactive compounds.

Published studies (Palinski et al., 1995, and George et al., 1998) have shown that immunisation against oxidised LDL reduces the development of atherosclerosis. This would indicate that immuno reactions against oxidised LDL in general have a protecting effect. The results given herein have, however, surprisingly shown that this is not always the case. E.g., immunisation using a mixture of peptides #10, 45, 154, 199, and 240 gave rise to an

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increase of the development of atherosclerosis. Immunisation using other peptide sequences, e.g., peptide sequences #1, and 30 to 34 lacks total effect on the development of atherosclerosis. The results are surprising because they provide basis for the fact that immuno reactions against oxidised LDL, can protect against the development, contribute to the development of atherosclerosis, and be without any effect at all depending on which structures in oxidised LDL they are directed to. These findings make it possible to develop immunisation methods, which isolate the activation of protecting immuno reactions. Further, they show that immunisation using intact oxidised LDL could have a detrimental effect if the particles used contain a high level of structures that give rise to atherogenic immuno reactions.

The technique of the present invention is based on quite different principles and methods. In accordance with claim 1 the invention relates to antibodies raised against oxidized fragments of apolipoprotein B, which antibodies are used for immunisation against cardiovascular disease.

As an alternative to active immunisation, using the identified peptides described above, passive immunisation with pre-made antibodies directed to the same peptides is an attractive possibility. Such antibodies may be given desired properties concerning e.g. specificity and crossreactivity, isotype, affinity and plasma halflife. The possibility to develop antibodies with predetermined properties became apparent already with the advent of the monoclonal antibody technology (Milstein and Köhler, 1975 Nature, 256:495-7). This technology used murine hybridoma cells producing large amounts of identical, but murine, antibodies. In fact, a large number of preclinical, and also clinical trials were started using murine monoclonal antibodies for treatment of e.g. cancers. However, due to the fact that the antibodies were of non-human origin the immune system of the patients recognised them as foreign and developed antibodies to them. As a consequence the efficacy and plasma half-lives of the murine antibodies were decreased, and often side effects from allergic reactions, caused by the foreign antibody, prevented successful treatment.

To solve these problems several approaches to reduce the murine component of the specific and potentially therapeutic antibody were taken. The first approach comprised technology to make so called chimearic antibodies where the murine variable domains of the antibody were transferred to human constant regions resulting in an antibody that was mainly human (Neuberger et al. 1985, Nature 314:268-70). A further refinement of this approach was to develop humanised antibodies where the regions of the murine antibody that contacted the antigen, the so called Complementarity Determining Regions (CDRs) were transferred to a human antibody framework. Such antibodies are almost completely human and seldom cause any harmful antibody responses when administered to patients. Several chimearic or humanised antibodies have been registered as therapeutic drugs and are now widely used within various indications (Borrebaeck and Carlsson, 2001, Curr. Opin. Pharmacol. 1:404-408).

Today also completely human antibodies may be produced using recombinant technologies. Typically large libraries comprising billions of different antibodies are used. In contrast to the previous technologies employing chimearisation or humanisation of e.g. murine antibodies this technology does not rely on immunisation of animals to generate the specific antibody. In stead the recombinant libraries comprise a huge number of pre-made antibody variants why it is likely that the library will have at least one antibody specific for any antigen. Thus, using such libraries the problem becomes the one to find the specific binder already existing in the library, and not to generate it through immunisations. In order to find the good binder in a library in an efficient manner, various systems where phenotype i.e. the antibody or antibody fragment is linked to its genotype i.e. the encoding gene have been devised. The most commonly used such system is the so called phage display system where antibody fragments are expressed, displayed, as fusions with phage coat proteins on the surface of filamentous phage particles, while simultaneously carrying the genetic information encoding the displayed molecule (McCafferty et al., 1990, Nature 348:552-554). Phage displaying antibody fragments specific for a particular antigen may be selected through binding to the antigen in question. Isolated phage may then be amplified and the gene encoding the selected antibody variable domains may optionally be transferred to other antibody formats as e.g. full length immunoglobulin and expressed in high amounts using appropriate vectors and host cells well known in the art.

The format of displayed antibody specificities on phage particles may differ. The most commonly used formats are Fab (Griffiths et al., 1994. EMBO J. *13*:3245-3260) and single chain (scFv) (Hoogenboom et al., 1992, J Mol Biol. *227*:381-388) both comprising the variable antigen binding domains of antibodies. The single chain format is composed of a variable heavy domain (VH) linked to a variable light domain (VL) via a flexible linker (US 4,946,778). Before use as analytical reagents, or therapeutic agents, the displayed antibody specificity is transferred to a soluble format e.g. Fab or scFv and analysed as such. In later steps the antibody fragment identified to have desireable characteristics may be transferred into yet other formats such as full length antibodies.

Recently a novel technology for generation of variability in antibody libraries was presented (WO98/32845, Soderlind et al., 2000, Nature BioTechnol. 18:852-856).

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Antibody fragments derived from this library all have the same framework regions and only differ in their CDRs. Since the framework regions are of germline sequence the immunogenicity of antibodies derived from the library, or similar libraies produced using the same technology, are expected to be particularly low (Soderlind et al., 2000, Nature BioTechnol. 18:852-856). This property is expected to be of great value for therapeutic antibodies reducing the risk for the patient to form antibodies to the administered antibody thereby reducing risks for allergic reactions, the occurrence of blocking antibodies, and allowing a long plasma half-life of the antibody. Several antibodies derived from recombinant libraries have now reached into the clinic and are expected to provide therapeutic drugs in the near future.

Thus, when met with the challenge to develop therapeutic antibodies to be used in humans the art teaches away from the earlier hybridoma technology and towards use of modern recombinant library technology (Soderlind et al., 2001, Comb. Chem. & High Throughput Screen. 4:409-416). It was realised that the peptides identified (PCT/SE02/00679), and being a integral part of this invention, could be used as antigens for generation of fully human antibodies with predetermined properties. In contrast to earlier art (US 6,225,070) the antigenic structures i.e. the peptides used in the present invention were identified as being particularly relevant as target sequences for therapeutic antibodies (PCT/SE02/00679). Also, in the present invention the antibodies are derived from antibody libraries omitting the need for immunisation of lipoprotein deficient mice to raise murine antibodies (US 6,225,070). Moreover, the resulting antibodies are fully human and are not expected to generate any undesired immunological reaction when administered into patients.

The peptides used, and previously identified (PCT/SE02/00679) are the following:

Table 1

A. High IgG, MDA-difference

P 11.	FLDTVYGNCSTHFTVKTRKG
P 25.	PQCSTHILQWLKRVHANPLL
P 74.	VISIPRLQAEARSEILAHWS

B. High IgM, no MDA-difference

P 40.	KLVKEALKESQLPTVMDFRK
P 68.	LKFVTQAEGAKQTEATMTFK
P 94.	DGSLRHKFLDSNIKFSHVEK
P 99.	KGTYGLSCQRDPNTGRLNGE
P 100.	RLNGESNLRFNSSYLQGTNQ
P 102.	SLTSTSDLQSGIIKNTASLK

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P 103.	TASLKYENYELTLKSDTNGK
P 105.	DMTFSKQNALLRSEYQADYE
P 177.	MKVKIIRTIDQMQNSELQWP

C. High IgG, no MDA difference

P 143.	IALDDAKINFNEKLSQLQTY
P 210.	KTTKQSFDLSVKAQYKKNKH

D. NHS/AHP, IgG-ak > 2, MDA-difference

P1.	EEEMLENVSLVCPKDATRFK
P 129.	GSTSHHLVSRKSISAALEHK
P 148.	IENIDFNKSGSSTASWIQNV
P 162.	IREVTQRLNGEIQALELPQK
P 252.	EVDVLTKYSQPEDSLIPFFE

E. NHS/AHP, IgM-ak > 2, MDA-difference

P 301.	HTFLIYITELLKKLQSTTVM
P 30.	LLDIANYLMEQIQDDCTGDE
P 31.	CTGDEDYTYKIKRVIGNMGQ
P 32.	GNMGQTMEQLTPELKSSILK
P 33.	SSILKCVQSTKPSLMIQKAA
P 34.	IQKAAIQALRKMEPKDKDQE
P 100.	RLNGESNLRFNSSYLQGTNQ
P 107.	SLNSHGLELNADILGTDKIN
P 149.	WIQNVDTKYQIRIQIQEKLQ
P 169.	TYISDWWTLAAKNLTDFAEQ
P 236.	EATLQRIYSLWEHSTKNHLQ

F. NHS/AHP, IgG-ak < 0.5,no MDA-difference

P 10.	ALLVPPETEEAKQVLFLDTV
P 45.	IEIGLEGKGFEPTLEALFGK
P 111.	SGASMKLTTNGRFREHNAKF
P 154.	NLIGDFEVAEKINAFRAKVH
P 199.	GHSVLTAKGMALFGEGKAEF
P 222.	FKSSVITLNTNAELFNQSDI
P 240.	FPDLGQEVALNANTKNQKIR

or an active site of one or more of these peptides.

In Table 1 above, the following is due:

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(A) Fragments that produce high levels of IgG antibodies to MDA-modified peptides (n=3),
(B) Fragments that produce high levels of IgM antibodies, but no difference between native an MDA-modified peptides (n=9),
(C) Fragments that produce high levels of IgG antibodies, but no difference between native an MDA-modified peptides (n=2),
(D) Fragments that produce high levels of IgG antibodies to MDA-modified peptides and at leas twice as much antibodies in the NHP-pool as compared to the AHP-pool (n=5),
(E) Fragments that produce high levels of IgM antibodies to MDA-modified peptides and at least twice as much antibodies in the NHP-pool as compared to the AHP-pool (n=11), and
(F) Fragments that produce high levels of IgG antibodies, but no difference between intact and MDA-modified peptides but at least twice as much antibodies in the AHP-pool as compared to the NHP-pool (n=7).

Summary of the invention

The present invention relates to the use of at least one recombinant human antibody or an antibody fragment thereof directed towards at least one oxidized fragment of apolipoprotein B in the manufacture of a pharmaceutical composition for therapeutical or prophylactical treatment of atherosclerosis by means of passive immunization.

Further the invention relates to the recombinant preparation of such antibodies, as well as the invention relates to method for passive immunization using such antibodies raised using an oxidized apolipoprotein B fragement, as antigen, in particular a fragemnt as identified above.

The present invention utilises a recombinant antibody fragment library to generate specific human antibody fragments against oxidized, in particular MDA modified peptides derived from Apo B100. Identified antibody fragments with desired characteristics may then rebuilt into full length human immunoglobulin to be used for therapeutic purposes.

Detailed description of the invention

Below will follow a detailed description of the invention examplified by, but not limited to, human antibodies derived from a recombinant antibody fragment library and directed towards two MDA modified peptides from ApoB 100.

Example 1.

Selection of scFv against MDA modified peptides IEIGL EGKGF EPTLE ALFGK (P45, Table 1) and KTTKQ SFDLS VKAQY KKNKH (P210, Table 1).

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The target antigens were chemically modified to carry Malone-di-aldehyde (MDA) groups on lysines and histidines. The modified peptides were denoted IEI (P45) and KTT (P210).

Selections were performed using BioInvent's n-CoDeR™*scFv* library for which the principle of construction and production have been described in Soderlind et al. 2000, Nature BioTechnology. 18, 852-856. The library contains approximately 2 x 10^{10} independent clones and a 2000 fold excess of clones were used as input for each selection. Selections were performed in three rounds. In selection round 1, Immunotubes (NUNC maxisorb 444202) were coated with 1.2 ml of 20 µg/ml MDA-modified target peptides in PBS (137 mM NaCl, 2.7 mM KCl, 4.3 mM Na_2HPO_4, 1.4 mM KH_2PO_4) with end over end agitation at +4°C over night. The tubes were then blocked with TPBSB5% (5 % BSA, 0.05% Tween 20, 0.02 % sodium Azide in PBS) for 30 minutes and washed twice with TPBSB3% (3 % BSA, 0.05% Tween 20, 0.02 % sodium Azide in PBS) before use. Each target tube was then incubated with approximately 2 x 10^{13} CFU phages from the n-CodeR™ library in 1.8 ml TPBSB3% for 2 h at room temperature, using end over end agitation. The tubes were then washed with 15 x 3 ml TPBSB3% and 2 x 1 ml PBS before the bound phages were eluted with 1 ml/tube of 2 mg/ml trypsin (Roche, 109819) for 30 minutes at room temperature. This procedure takes advantage of a specific trypsin site in the scFv-fusion protein to release the phage from the target. The reaction was stopped by the addition of 100 µl of Aprotein (0.2 mg/ml, Roche, cat.236624), and the Immunotubes were washed with 300 ul PBS, giving a final volume of 1.4 ml.

For amplification of the selected phage E. *Coli* HB101F' cells were grown exponentially in 10 ml of LB medium (Merck, cat. 1.10285) to $OD_{600} = 0.5$ and infected with the selected and eluted phage principally as described (Soderlind et al., 2000, Nature BioTechnol. 18, 852-856. The resulting phage supernatant was then precipitated by addition of 1/4 volume of 20% PEG_{6000} in 2.5 M NaCl and incubated for 5 h at +4°C. The phages were then pelleted by centrifugation for 30 minutes, 13000 x g, re-suspended in 500 µl PBS and used in selection round 2.

The amplified phagestock was used in selection round 2 in a final volume of 1.5 ml of 5 % BSA, 0.05% Tween 20, 0.02 % sodium Azide in PBS. Peptide without MDA modification (4 x 10^{-7} M) was also included for competition against binders to MDA-unmodified target peptide. The mixture was incubated in Immunotubes prepared with antigen as described above, except that the tubes were blocked with 1 % Casein instead of TPBSB3%. The incubations and washing of the Immunotubes were as described for selection 1. Bound phages were then eluted for 30 minutes using 600 µl of 100 mM Tris-

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Glycine buffer, pH 2.2. The tubes were washed with additional 200 µl glycin buffer and the eluates were pooled and then neutralised with 96 µl of 1 M Tris-HCl, pH 8.0. The samples were re-natured for 1 h at room temperature and used for selection round 3.

For selection round 3, BSA, Tween 20 and Sodium Azide were added to the renaturated phage pool to a final concentration of 3 %, 0.05% and 0.02%, respectively. Competitor peptides, MDA modified unrelated peptides as well as native target peptides without modification were added to a concentration of 1×10^{-7}M. The phage mixtures (1100 µl) were added to immunotubes coated with target antigen as described in selection 1 and incubated over night at 4°C with agitation. The tubes were then washed with 3 x 3 ml TPBSB 3%, 5 x 3 ml PBS and eventually bound phages were eluted using trypsin as described in selection round 1 above. Each eluate was infected to 10 ml of logarithmically growing HB101F' in LB containing 100 µg/ml ampicillin, 15 µg/ml tetracycline, 0.1% glucose, and grown over night at 30°C, 200 rpm in a shaker incubator.

The over night cultures were used for mini scale preparation of plasmid DNA, using Biorad mini prepp Kit (Cat. 732 6100). To remove the phage gene III part from the expression vector, 0.25 µg of the plasmid DNA was cut for 2 h at 37°C using 2.5 U Eag-1 (New England Biolabs, cat. R050) in the buffer recommended by the supplier. The samples were then heat inactivated for 20 minutes at 65°C and ligated over night at 16°C using 1 U T4 DNA ligase in 30 µl of 1 x ligase buffer (Gibco/BRL). This procedure will join two Eag-1 sites situated on opposite sides of the phage gene III fragment, thus creating a free scFv displaying a terminal 6xhis tag. After ligation the material was digested for 2 h at 37°C in a solution containing 30 ul ligation mix, 3.6 µl 10 x REACT3 stock, 0.4 µl 1 M NaCl, 5 µl H_2O_2, in order to destroy clones in which the phage gene III segment had been religated. Twenty (20) ng of the final product were transformed into chemical competent Top10F' and spread on 500 cm^2 Q-tray LA-plates (100 µg/ml Amp, 1% glucose), to enable the picking of single colonies for further screening.

Screening of the n-CoDeR™scFv library for specific antibody fragments binding t0 MDA modified peptides from Apolipoprotein B-100

In order to identify scFv that could discriminate between MDA modified IEI (P45) peptide and native IEI and between MDA modified KTT (P210) and native KTT respectively screenings were performed on bacterial supernatants from selected scFv expressing clones.

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Colony picking of single clones, expression of scFv and screening number 1 was performed on BioInvent's automatic system according to standard methods. 1088 and 831 single clones selected against the MDA modified IEI and KTT peptides respectively

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Table 2. Screening results. The number of clones tested in each screening step for each target. The scored hits in percent are shown within brackets.

		Target	
		IEI	KTT
Screening number 1	Tested Clones	1088	831
	Scored Hits (%)	64 (5.9%)	33 (4.0%)
Screening number 2	Tested Clones	64	33
	Scored Hits (%)	12 (1.1%)	2 (0.2%)
Dose response	Tested Clones	12	2
	Scored Hits (%)	8 (0.7%)	2 (0.2%)

The sequences of the chosen scFv clones were determined in order to find unique clones. Bacterial PCR was performed with the Boeringer Mannheim Expand kit using primers (5'-CCC AGT CAC GAC GTT GTA AAA CG-3') and (5'-GAA ACA GCT ATG AAA TAC CTA TTG C-3') and a GeneAmp PCR system 9700 (PE Applied system) using the temperature cycling program 94°C 5 min, 30 cycles of 94°C 30s, 52°C for 30s and 68°C for 2min and finally 5 min at 68 min. The sequencing reaction was performed with the bacterial PCR product (five fold diluted) as template, using Big Dye Terminator mix from PE Applied Biosystems and the GeneAmp PCR system 9700 (PE Applied system) and the temperature cycling program 25 cycles of 96°C 10s, 50°C for 5s and 60°C for 4 min. The extension products were purified according to the supplier's instructions and the separation and detection of extension products was done by using a 3100 Genetic analyser (PE Applied Biosystems). The sequences were analysed by the in house computer program. From the sequence information homologous clones and clones with inappropriate restriction sites were excluded, leaving six clones for IgG conversion. The DNA sequence of the variable heavy (VH) and variable light (VL) domains of the finally selected clones are shown in Figure 3.

Example 2.

Transfer of genes encoding the variable parts of selected scFv to full length human IgG1 vestors.

Bacteria containing scFv clones to be converted to Ig-format were grown over night in LB supplemented with 100 μg/ml ampicillin. Plasmid DNA was prepared from over night cultures using the Quantum Prep, plasmid miniprep kit from Biorad (# 732-6100). The DNA concentration was estimated by measuring absorbance at 260nm, and the DNA was diluted to a concentration of 2 ng/μl.

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VH and VL from the different scFv-plasmids were PCR amplified in order to supply these segments with restriction sites compatible with the expression vectors (see below). 5' primers contain a BsmI and 3' primers contain a BsiWI restriction enzyme cleavage site (shown in italics). 3' primers also contained a splice donor site (shown in bold).

Primers for amplification of VH-segments:
5'VH: 5'-GGT*GTGCATTC*CGAGGTGCAGCTGTTGGAG (SEQ. ID. NO: 13)
3'VH: 5'-GA*CGTACG***ACTCACCT**GAGCTCACGGTGACCAG (SEQ. ID. NO: 14)

Primers for amplification of VL-segments:
5'VL: 5'-GGT*GTGCATTC*CCAGTCTGTGCTGACTCAG (SEQ. ID. NO: 15)
3'VL: 5'-GA*CGTACG*TTCT**ACTCACCT**AGGACCGTCAGCTT (SEQ. ID. NO: 16)

PCR was conducted in a total volume of 50 µl, containing 10ng template DNA, 0.4 µM 5' primer, 0.4 µM 3' primer and 0.6 mM dNTP (Roche, #1 969 064). The polymerase used was Expand long template PCR system (Roche # 1 759 060), 3.5 u per reaction, together with each of the supplied buffers in 3 separate reactions. Each PCR amplification cycle consisted of a denaturing step at 94°C for 30 seconds, an annealing step at 55°C for 30 seconds, and an elongating step at 68°C for 1.5 minutes. This amplification cycle was repeated 25 times. Each reaction began with a single denaturing step at 94°C for 2 minutes and ended with a single elongating step at 68°C for 10 minutes. The existence of PCR product was checked by agarose gel electrophoresis, and reactions containing the same amplified material (from reactions with different buffers) were pooled. The PCR amplification products were subsequently purified by spin column chromatography using S400-HR columns (Amersham-Pharmacia Biotech # 27-5240-01).

Four (4) µl of from each pool of PCR products were used for TOPO TA cloning (pCR 2.1 TOPO, InVitrogen #K4550-01) according to the manufacturers recommendations. Bacterial colonies containing plasmids with inserts were grown over night in LB supplemented with 100 µg/ml ampicillin and 20 µg/ml kanamycin. Plasmid DNA was prepared from over night cultures using the Quantum Prep, plasmid miniprep kit from Biorad (# 732-6100). Plasmid preparations were purified by spin column chromatography using S400-HR columns (Amersham-Pharmacia Biotech # 27-5240-01). Three plasmids from each individual VH and VL cloning were subjected to sequence analysis using BigDye Cycle Sequencing (Perkin Elmer Applied Biosystem, # 4303150). The cycle sequencing program consisted of a denaturing step at 96°C for 10 seconds, an annealing step at 50°C for 15 seconds, and an elongating step at 60°C for 4 minutes. This cycle was repeated 25 times. Each reaction began with a single denaturing step at

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94°C for 1 minute. The reactions were performed in a volume of 10 µl consisting of 1 µM primer (5'-CAGGAAACAGCTATGAC), 3 µl plasmid DNA and 4 µl Big Dye reaction mix. The reactions were precipitated according to the manufacturers recommendations, and samples were run on a ABI PRISM 3100 Genetic Analyzer. Sequences were compared to the original scFv sequence using the alignment function of the OMIGA sequence analysis software (Oxford Molecular Ltd).

Plasmids containing VH and VL segments without mutations were restriction enzyme digested. To disrupt the pCR 2.1 TOPO vector, plasmids were initially digested with DraI (Roche # 1 417 983) at 37°C for 2 hours. Digestions were heat inactivated at 70°C for 20 minutes and purified by spin column chromatography using S400-HR columns (Amersham-Pharmacia Biotech # 27-5240-01). The purified DraI digestions were subsequently digested with BsmI (Roche # 1 292 307) and BsiWI (Roche # 1 388 959) at 55°C over night. Digestions were purified using phenol extraction and precipitation. The precipitated DNA was dissolved in 10 µl H_2O and used for ligation.

The expression vectors were obtained from Lars Norderhaug (J. Immunol. Meth. 204 (1997) 77-87). After some modifications, the vectors (Figure 4) contain a CMV promoter, an Ig-leader peptide, a cloning linker containing BsmI and BsiWI restriction sites for cloning of VH/VL, genomic constant regions of IgG1(heavy chain (HC) vector) or lambda (light chain (LC) vector), neomycin (HC vector) or methotrexate (LC vector) resistance genes for selection in eukaryotic cells, SV40 and ColEI origins of replication and ampicillin (HC vector) or kanamycin (LC vector) resistance genes for selection in bacteria.

The HC and LC vectors were digested with BsmI and BsiWI, phosphatase treated and purified using phenol extraction and precipitation. Ligation were set up at 16°C over night in a volume of 10 µl, containing 100 ng digested vector, 2 µl digested VH/VL-pCR 2.1 TOPO vector (see above), 1 U T4 DNA ligase (Life Technologies, # 15224-025) and the supplied buffer. 2 µl of the ligation mixture were subsequently transformed into 50 µl chemocompetent top10F' bacteria, and plated on selective (100 µg/ml ampicillin or 20 µg/ml kanamycin) agar plates.

Colonies containing HC/LC plasmids with VH/VL inserts were identified by colony PCR:
Forward primer: 5'-ATGGGTGACAATGACATC
Reverse primer: 5'-AAGCTTGCTAGCGTACG

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PCR was conducted in a total volume of 20 µl, containing bacterias, 0.5 µM forward primer, 0.5 µM reverse primer and 0.5 mM dNTP (Roche, #1 969 064). The polymerase used was Expand long template PCR system (Roche # 1 759 060), 0.7 U per reaction, together with the supplied buffer #3. Each PCR amplification cycle consisted of a denaturing step at 94°C for 30 seconds, an annealing step at 52°C for 30 seconds, and an elongating step at 68°C for 1.5 minutes. This amplification cycle was repeated 30 times. Each reaction began with a single denaturing step at 94°C for 2 minutes and ended with a single elongating step at 68°C for 5 minutes. The existence of PCR product was checked by agarose gel electrophoresis. Colonies containing HC/LC plasmids with VH/VL inserts were grown over night in LB supplemented with 100 µg/ml ampicillin or 20 µg/ml kanamycin. Plasmid DNA was prepared from over night cultures using the Quantum Prep, plasmid miniprep kit from Biorad (# 732-6100). Plasmid preparations were purified by spin column chromatography using S400-HR columns (Amersham-Pharmacia Biotech # 27-5240-01). To confirm the integrity of the DNA sequence, three plasmids from each individual VH and VL were subjected to sequence analysis using BigDye Cycle Sequencing (Perkin Elmer Applied Biosystem, # 4303150). The cycle sequencing program consisted of a denaturing step at 96°C for 10 seconds, an annealing step at 50°C for 15 seconds, and an elongating step at 60°C for 4 minutes. This cycle was repeated 25 times. Each reaction began with a single denaturing step at 94°C for 1 minute. The reactions were performed in a volume of 10 µl consisting of 1 µM primer (5'-AGACCCAAGCTAGCTTGGTAC), 3µl plasmid DNA and 4µl Big Dye reaction mix. The reactions were precipitated according to the manufacturers recommendations, and samples were run on a ABI PRISM 3100 Genetic Analyzer. Sequences were analysed using the OMIGA sequence analysis software (Oxford Molecular Ltd). The plasmid DNA was used for transient transfection of COS-7 cells (see below) and were digested for production of a joined vector, containing heavy- and light chain genes on the same plasmid.

Heavy and light chain vectors containing VH and VL segments originating from the same scFv were cleaved by restriction enzymes and ligated: HC- and LC-vectors were initially digested with MunI (Roche # 1 441 337) after which digestions were heat inactivated at 70°C for 20 minutes and purified by spin column chromatography using S200-HR columns (Amersham-Pharmacia Biotech # 27-5120-01). HC-vector digestions were subsequently digested with NruI (Roche # 776 769) and LC-vector digestions with Bst1107I (Roche # 1 378 953). Digestions were then heat inactivated at 70°C for 20 minutes and purified by spin column chromatography using S400-HR columns (Amersham-Pharmacia Biotech # 27-5240-01). 5 µl of each digested plasmid were ligated at 16°C over night in a total volume of 20 µl, contaning 2 U T4 DNA ligase (Life

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Technologies, # 15224-025) and the supplied buffer. 2 µl of the ligation mixture were subsequently transformed into 50 µl chemocompetent top10F' bacteria, and plated on selective (100 µg/ml ampicillin and 20 µg/ml kanamycin) agar plates.

Bacterial colonies were grown over night in LB supplemented with 100 µg/ml ampicillin and 20 µg/ml kanamycin. Plasmid DNA was prepared from over night cultures using the Quantum Prep, plasmid miniprep kit from Biorad (# 732-6100). Correctly joined vectors were identified by restriction enzyme digestion followed by analyses of fragment sizes by agarose gel-electrophoreses

Plasmid preparations were purified by spin column chromatography using S400-HR columns (Amersham-Pharmacia Biotech # 27-5240-01) and used for transient transfection of COS-7 cells.

COS-7 cells (ATCC # CRL-1651) were cultured at 37°C with 5% CO_2 in Dulbeccos MEM, high glucose + GlutamaxI (Invitrogen # 31966021), supplementd with 0.1 mM non-essential amino acids (Invitrogen # 11140035) and 10% fetal bovine sera (Invitrogen # 12476-024, batch # 1128016). The day before transfection, the cells were plated in 12-well plates (Nunc, # 150628) at a density of $1.5x10^5$ cells per well.

Prior to transfection, the plasmid DNA was heated at 70°C for 15 minutes. Cells were transfected with 1 µg HC-plasmid + 1 µg LC-plasmid, or 2 µg joined plasmid per well, using Lipofectamine 2000 Reagent (Invitrogen, # 11668019) according to the manufacturers recommendations. 24 hours post transfection, cell culture media was changed and the cells were allowed to grow for 5 days. After that, medium was collected and protein production was assayed for using ELISA.

Ninetysix (96)-well plates (Costar # 9018, flat bottom, high binding) were coated at 4°C over night by adding 100 µl/well rabbit anti-human lamda light chain antibody (DAKO, # A0193) diluted 4000 times in coatingbuffer (0.1M sodium carbonate, pH 9.5). Plates were washed 4 times in PBS containing 0.05% Tween 20 and thereafter blocked with 100 µl/well PBS+3% BSA (Albumin, fraction V, Roche # 735108) for 1 h. at room temperature. After washing as above, 100 µl/well of sample were added and incubated in room temperature for 1 hour. As a standard for estimation of concentration, human purified IgG1 (Sigma, # I5029) was used. Samples and standard were diluted in sample buffer (1x PBS containing 2% BSA and 0.5% rabbit serum (Sigma # R4505). Subsequently, plates were washed as described above and 100 µl/well of rabbit anti-human IgG (γ-chain) HRP-conjugated antibody (DAKO, # P214) diluted 8000 times in

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sample buffer was added and incubated at room temperature for 1 hour. After washing 8 times with PBS containing 0.05% Tween 20, 100 µl/well of a substrate solution containing one OPD tablet (10 mg, Sigma # P8287,) dissolved in 15 ml citric acid buffer and 4.5 µl H_2O_2 (30%) was added. After 10 minutes, the reaction was terminated by adding 150 µl/well of 1M HCl. Absorbance was measured at 490-650 nm and data was analyzed using the Softmax software.

Bacteria containing correctly joined HC- and LC-vectors were grown over night in 500 ml LB supplemented with ampicillin and kanamycin. Plasmid DNA was prepared from over night cultures using the Quantum Prep, plasmid maxiprep kit from Biorad (# 732-6130). Vectors were linearized using PvuI restriction enzyme (Roche # 650 129). Prior to transfection, the linearized DNA was purified by spin column chromatography using S400-HR columns (Amersham-Pharmacia Biotech # 27-5240-01) and heated at 70°C for 15 minutes.

Example 3

Stable transfection of NS0 cells expressing antibodies against MDA modified peptides frm Apolipoprotein B-100.

NS0 cells (ECACC no. 85110503) were cultured in DMEM (cat nr 31966-021, Invitrogen) supplemented with 10% Fetal Bovine Serum (cat no. 12476-024, lot: 1128016, Invitrogen) and 1X NEAA (non-essential amino acids, cat no. 11140-053, Invitrogen). Cell cultures are maintained at 37°C with 5% CO_2 in humidified environment.

DNA constructs to be transfected were four constructs of IEI specific antibodies (IEI-A8, IEI-D8, IEI-E3, IEI-G8), two of KTT specific antibodies (KTT-B8, KTT-D6) and one control antibody (JFPA12).The day before transfection, the cells were trypsinized and counted, before plating them in a T-75 flask at $12x10^6$cells/flask. On the day of transfection, when the cells were 85-90% confluent, the cells were plated in 15 ml DMEM + 1X NEAA + 10 % FBS (as above). For each flask of cells to be transfected, 35-40 µg of DNA were diluted into 1.9 ml of OPTI-MEM I Reduced Serum Medium (Cat no. 51985-026, lot: 3062314, Invitrogen) without serum. For each flask of cells, 114 µl of Lipofectamine 2000 Reagent (Cat nr. 11668-019, lot: 1116546, Invitrogen) were diluted into 1.9 ml OPTI-MEM I Reduced Serum Medium in another tube and incubated for 5 min at room temperature. The diluted DNA was combined with the diluted Lipofectamine 2000 Reagent (within 30 min) and incubated at room temperature for 20 min to allow DNA-LF2000 Reagent complexes to form.

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The cells were washed with medium once and 11 ml DMEM + 1X NEAA + 10 % FBS were added. The DNA-LF2000 Reagent complexes (3.8 ml) were then added directly to each flask and gently mixed by rocking the flask back and forth. The cells were incubated at 37 °C in a 5% CO_2 incubator for 24 h.

The cells were then trypsinized and counted, and subsequently plated in 96-well plates at $2x10^4$ cells/well using five 96-well plates/construct. Cells were plated in 100 µl/well of DMEM + 1X NEAA + 10 % FBS (as above) containing G418-sulphate (cat nr.10131-027, lot: 3066651, Invitrogen) at 600 µg/ml. The selection pressure was kept unchanged until harvest of the cells.

The cells were grown for 12 days and assayed for antibody production using ELISA. From each construct cells from the 24 wells containing the highest amounts of IgG were transferred to 24-well plates and were allowed to reach confluency. The antibody production from cells in these wells was then assayed with ELISA and 5-21 pools/construct were selected for re-screening (Table 3). Finally cells from the best 1-4 wells for each construct were chosen. These cells were expanded successively in cell culture flasks and finally transferred into triple layer flasks (500 cm2) in 200 ml of (DMEM + 1xNEAA + 10% Ultra low IgG FBS (cat.no. 16250-078, lot.no. 113466, Invitrogen) + G418 (600 µg/ml)) for antibody production. The cells were incubated for 7-10 days and the supernatants were assayed by ELISA, harvested and sterile filtered for purification.

Example 4.

Production and purification of human IgG1

Supernatants from NS0 cells transfected with the different IgG1 antibodies were sterile filtered using a 0.22 µm filter and purified using an affinity medium MabSelect™ with recombinant protein A, (Cat. No. 17519901 Amersham Biosciences).

Bound human IgG1 was eluted with HCL-glycine buffer pH 2.8. The eluate was collected in 0.5 ml fractions and OD_{280} was used to determine presence of protein. The peak fractions were pooled and absorbance was measured at 280nm and 320nm. Buffer was changed through dialysis against a large volume of PBS. The presence of endotoxins in the purified IgG-1 preparations was tested using a LAL test (QCL-1000^R, cat. No. 50-647U Bio Whittaker). The samples contained between 1 and 12 EU/ml endotoxin. The purity of the preparations were estimated to exceed 98% by PAGE analysis.

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Table 3 Summary of Production and Purification of human IgG1

Clone name	Volume culture supernatant (ml)	Total IgG1 in supernatant (mg)	Total IgG1 Purified (mg)	Yield (%)
IEI-A8	600	68	42	61.8
IEI-D8	700	45	21	46.7
IEI-E3	700	44.9	25.6	60
IEI-G8	600	74	42.4	57.3
KTT-B8	1790	77.3	37.6	48.6
KTT-D6	1845	47.8	31.8	66.5
JFPA12	2000	32.2	19.2	59.6

The purified IgG1 preparations were tested in ELISA for reactivity to MDA modified and un-modified peptides (Figure 5) and were then used in functional in vitro and in vivo studies.

Example 5.

Analysis of possible anti-atherogenic effect of antibodies are performed both in experimental animals and in cell culture studies.

1. *Effect of antibodies on atherosclerosis in apolipoprotein E knockout (apo E-) mice.* Five weeks old apo E- mice are fed a cholesterol-rich diet for 15 weeks. This treatment is known to produce a significant amount of atherosclerotic plaques in the aorta and carotid arteries. The mice are then given an intraperitoneal injection containing 500 µg of the respective antibody identified above. Control mice are given 500 µg of an irrelevant control antibody or PBS alone. Treatments are repeated after 1 and 2 weeks. The mice are sacrificed 4 weeks after the initial antibody injection. The severity of atherosclerosis in the aorta is determined by Oil Red O staining of flat preparations and by determining the size of subvalvular atherosclerotic plaques. Collagen, macrophage and T cell content of subvalvular atherosclerotic plaques is determined by Masson trichrome staining and cell-specific immunohistochemistry. Quantification of Oil Red O staining, the size of the subvalvular plaques, trichrome staining and immunohistochemical staining is done using computer-based image analysis.

In a first experiment the effect of the antibodies on development of atherosclerosis was analysed in apo E-/- mice fed a high-cholesterol diet. The mice were given three intraperitoneal injections of 0.5 mg antibody with week intervals starting at 21 weeks of age, using PBS as control. They were sacrificed two weeks after the last antibody

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injection, and the extent of atherosclerosis was assessed by Oil Red O staining of descending aorta flat preparations. A pronounced effect was observed in mice treated with the IEI-E3 antibody, with more than 50% reduction of atherosclerosis as compared to the PBS group (*P*=0.02) and to a control group receiving a human IgG1 antibody (FITC8) directed against a non-relevant fluorescein isothiocynate (FITC) antigen (P=0.03) (Fig. 6). The mice tolerated the human antibodies well and no effects on the general health status of the mice were evident.

To verify the inhibitory effect of the IEI-E3 antibody on development of atherosclerosis we then performed a dose-response study. The schedule was identical to that of the initial study. In mice treated with IEI-E3 antibodies atherosclerosis was reduced by 2% in the 0.25 mg group (n.s.), by 25% in the 0.5 mg group (n.s.) and by 41% (*P*=0.02) in the 2.0 mg group as compared to the corresponding FITC antibody-treated groups (Fig. 7).

2. Effect of antibodies on neo-intima formation following mechanical injury of carotid arteries in apo E- mice. Mechanical injury of arteries results in development of fibro-muscular neo-intimal plaque within 3 weeks. This plaque resembles morphologically a fibro-muscular atherosclerotic plaque and has been used as one model for studies of the development of raised lesion. Placing a plastic collar around the carotid artery causes the mechanical injury. Five weeks old apo E- mice are fed a cholesterol-rich diet for 14 weeks. The mice are then given an intraperitoneal injection containing 500 µg of the respective antibody. Control mice are given 500 µg of an irrelevant control antibody or PBS alone. The treatment is repeated after 7 days and the surgical placement of the plastic collar is performed 1 day later. A last injection of antibodies or PBS is given 6 days after surgery and the animals are sacrificed 15 days later. The injured carotid artery is fixed, embedded in paraffin and sectioned. The size of the neo-intimal plaque is measured using computer-based image analysis.

3. *Effect of antibodies on uptake of oxidized LDL in cultured human macrophages.* Uptake of oxidized LDL in arterial macrophages leading to formation of cholesterol-loaded macrophage foam cells is one of the most characteristic features of the atherosclerotic plaque. Several lines of evidence suggest that inhibiting uptake of oxidized LDL in arterial macrophages represent a possible target for treatment of atherosclerosis. To study the effect of antibodies on macrophage uptake of oxidized c are pre-incubated with ^{125}I-labeled human oxidized LDL for 2 hours. Human macrophages are isolated from blood donor buffy coats by centrifugation in Ficoll

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hypaque followed by culture in presence of 10% serum for 6 days. The cells are then incubated with medium containing antibody/oxidized LDL complexes for 6 hours, washed and cell-associated radioactivity determined in a gamma-counter. Addition of IEI-E3 antibodies resulted in a five-fold increase in the binding (P=0.001) and uptake (P=0.004) of oxidized LDL compared to FITC-8 into macrophages, but had no effect on binding or uptake of native LDL (Fig. 8a and 8b).

4. *Effect of antibodies on oxidized LDL-dependent cytotoxicity.* Oxidized LDL is highly cytotoxic. It is believed that much of the inflammatory activity in atherosclerotic plaques is explained by cell injury caused by oxidized LDL. Inhibition of oxidized LDL cytotoxicity thus represents another possible target for treatment of atherosclerosis. To study the effect of antibodies on oxidized LDL cytotoxicity cultured human arterial smooth muscle cells are exposed to 100 ng/ml of human oxidized LDL in the presence of increasing concentrations of antibodies (0-200 ng/ml) for 48 hours. The rate of cell injury is determined by measuring the release of the enzyme LDH.

The experiment shown discloses an effect for a particular antibody raised against a particular peptide, but it is evident to the one skilled in the art that all other antibodies raised against the peptides disclosed will behave in the same manner.

The antibodies of the present invention are used in pharmaceutical compositions for passive immunization, whereby the pharmaceutical compositions primarily are intended for injection, comprising a solution, suspension, or emulsion of a single antibody or a mixture of antibodies of the invention in a dosage to provide a therapeutically or prophylactically active level in the body treated. The compositions may be provided with commonly used adjuvants to enhance absorption of the antibody or mixture of antibodies. Other routes of administration may be the nasal route by inhaling the antibody/antibody mixture in combination with inhalable excipients.

Such pharmaceutical compositions may contain the active antibody in an amount of 0.5 to 99.5 % by weight, or 5 to 90 % by weight, or 10 to 90 % by weight, or 25 to 80 % by weight, or 40 to 90 % by weight.

The daily dosage of the antibody, or a booster dosage shall provide for a therapeutically or prophylactically active level in the body treated to reduce or prevent signs and sympthoms of atherosclerosis by way of passive immunization. A dosage of antibody according to the invention may be 1 μg to 1 mg per kg bodyweight, or more.

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The antibody composition can be supplemented with other drugs for treating or preventing atherosclerosis or heart-vascular diseases, such as blood pressure lowering drugs, such as beta-receptor blockers, calcium antagonists, diurethics, and other antihypertensive agents.

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CLAIMS

1. Use of at least one recombinant human antibody or antibody fragment directed towards at least one oxidized fragment of apolipoprotein B in the manufacture of a pharmaceutical composition for therapeutical or prophylactical treatment of atherosclerosis by means of passive immunization.

2. Use according to claim 1, wherein the oxidized fragment is selected from one or more of the group consisting of
FLDTVYGNCSTHFTVKTRKG
PQCSTHILQWLKRVHANPLL
VISIPRLQAEARSEILAHWS
KLVKEALKESQLPTVMDFRK
LKFVTQAEGAKQTEATMTFK
DGSLRHKFLDSNIKFSHVEK
KGTYGLSCQRDPNTGRLNGE
RLNGESNLRFNSSYLQGTNQ
SLTSTSDLQSGIIKNTASLK
TASLKYENYELTLKSDTNGK
DMTFSKQNALLRSEYQADYE
MKVKIIRTIDQMQNSELQWP
IALDDAKINFNEKLSQLQTY
KTTKQSFDLSVKAQYKKNKH
EEEMLENVSLVCPKDATRFK
GSTSHHLVSRKSISAALEHK
IENIDFNKSGSSTASWIQNV
IREVTQRLNGEIQALELPQK
EVDVLTKYSQPEDSLIPFFE
HTFLIYITELLKKLQSTTVM
LLDIANYLMEQIQDDCTGDE
CTGDEDYTYKIKRVIGNMGQ
GNMGQTMEQLTPELKSSILK
SSILKCVQSTKPSLMIQKAA
IQKAAIQALRKMEPKDKDQE
RLNGESNLRFNSSYLQGTNQ
SLNSHGLELNADILGTDKIN
WIQNVDTKYQIRIQIQEKLQ
TYISDWWTLAAKNLTDFAEQ
EATLQRIYSLWEHSTKNHLQ

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ALLVPPETEEAKQVLFLDTV
IEIGLEGKGFEPTLEALFGK
SGASMKLTTNGRFREHNAKF
NLIGDFEVAEKINAFRAKVH
GHSVLTAKGMALFGEGKAEF
FKSSVITLNTNAELFNQSDI
FPDLGQEVALNANTKNQKIR,
or an active site thereof.

3. Use according to claims 1-2, wherein the fragment has been oxidized using malone dealdehyde.

4. Use according to claims 1-2, wherein the fragment has been oxidized using copper.

5. Use according to claims 1-4, wherein the antibody is characterized in that it comprises the variable heavy region(V_H)

gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcac
cttcaataacgcctggatgagctgggtccgccaggctccagggaaggggctggagtgggtctcatccattagtagtagtagt
agttacatatactacgcagactcagtgaagggccgattcaccatctccagagacaattccaagaacacgctgtatctgcaaat
gaacagcctgagagccgaggacactgccgtgtattactgtgcgagagtcagtaggtactactacggaccatctttctactttga
ctcctggggccagggtacactggtcaccgtgagcagc

and the variable light region (V_L)

cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgctctggaagcaggtccaa
cattgggaataattatgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctatggtaacaacaatcggcc
ctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatga
ggctgattattactgtgcagcatgggatgacagcctgaatggtcattgggtgttcggcggaggaaccaagctgacggtccta
ggt.

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6. Use according to claims 1-4, wherein the antibody is characterized in that it comprises the variable heavy region (V_H)

gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcggcctctggattcac
cttcagtgactactacatgagctgggtccgccaggctcccgggaaggggctggagtgggtatcgggtgttagttggaatggc
agtaggacgcactatgcagactctgtgaagggccgattcaccatctccagagacaattccaagaacacgctgtatctgcaaat
gaacagcctgagagccgaggacactgccgtgtattactgtgcgagagcggctaggtactcctactactactacggtatggac
gtctggggccaaggtacactggtcaccgtgagcagc

and the variable light region (V_L)

cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgttctggaagcagctccaa
catcggaaataatgctgtaaactggtatcagcagctcccaggaacggcccccaaactcctcatctatgggaatgatcggcgg
ccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggat
gaggctgattattactgtcagacctggggcactggccgggggtattcggcggaggaaccaagctgacggtcctaggt

7. Use according to claims 1-4, wherein the antibody is characterized in that it comprises the variable heavy region (V_H)

gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcac
ctttagtagctattggatgagctgggtccgccaggctccagggaaggggctggagtgggtctcaagtatcagtggtagtggtc
gtaggacatactacgcagactccgtgcagggccggttcaccatctccagagacaattccaagaacacgctgtatctgcaaatg
aacagcctgagagccgaggacactgccgtgtattactgtgcgagattggtctcctatggttcggggagtttcggttttgactact
ggggccaaggtacactggtcaccgtgagcagc

and the variable light region (V_L)

cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaat
atcggaagtaattatgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctatggtaactacaatcggccc
tcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatgag
gctgattattactgtgcagcatgggatgacagcctgagtggttgggtgttcggcggaggaaccaagctgacggtcctaggt

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8. Use according to claims 1-4, wherein the antibody is characterized in that it comprises the variable heavy region (V_H)

gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcac
cttcagtaacgcctggatgagctgggtccgccaggttccagggaaggggctggagtgggtctcaactcttggtggtagtggt
ggtggtagcacatactacgcagactccgtgaagggccggttcaccatctccagagacaattccaagaacacgctgtatctgc
aaatgaacagcctgagagccgaggacactgccgtgtattactgtgcgaagttagggggcgatcccgatatgggcggtggc
cccgccaatttgactactggggccaaggtacactggtcaccgtgagcagc

and the variable light region (V_L)

cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgctctggaagcagctccaa
cattggaaataactatgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggcc
ctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatga
ggctgattattactgtgcagcatgggatgacagcctgagtcattggctgttcggcggaggaaccaagctgacggtcctaggt

9. Use according to claims 1-4, wherein the antibody is characterized in that it comprises the variable heavy region (V_H)

gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcac
cttcagtgactactacatgagctggatccgccaggctccagggaaggggctggagtgggtctcaagtatcagtggccgtggg
ggtagttcctactacgcagactccgtgaggggccggttcaccatctccagagacaattccaagaacacgctgtatctgcaaat
gaacagcctgagagccgaggacactgccgtgtattactgtgcgagactttcctacagctatggttacgagggggcctactact
ttgactactggggccagggtacactggtcaccgtgagcagc

and the variable light region (V_L)

cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgctctggaagcagctccaa
cattgggaataattatgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctataggaataatcagcggcc
ctcaggggtccctgaccgattctctggctccaagtctggcaccttagcctccctggccatcagtgggctccggtccgaggatga
ggctgattattactgtgcaacctgggatgacagcctgaatggttgggtgttcggcggaggaaccaagctgacggtcctaggt

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10. Use according to claims 1-4, wherein the antibody is characterized in that it comprises
the variable heavy region (V_H)

gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcac
ctttagcagctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcatccattagtagtagtggtc
gtttcatttactacgcagactcaatgaagggccgcttcaccatctccagagacaattccaagaacacgctgtatctgcaaatga
acagcctgagagccgaggacactgccgtgtattactgtacgaggctccggagagggagctacttctgggcttttgatatctgg
ggccaaggtacactggtcaccgtgagcagc

and the variable light region (V_L)

cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgttctggaagcagctccaa
cattggcggtgagtctgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggcc
ctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatga
ggctgattattactgtgcagcatgggatgacagcctgaatggttgggtgttcggcggaggaaccaagctgacggtcctaggt

11. Method for preparation of a recombinant antibody according to claims 1-10, using a fragment library to generate specific human antibody fragments against oxidized, in particular MDA modified peptides derived from Apo B100, whereupon identified antibody fragments having the desired characteristics are rebuilt into full length human immunoglobulin to be used for therapeutic purposes.

12. Method for amplification of a recombinant human antibody according to claim 11, using a recombinant technology, comprising transfer of genes encoding the variable parts of selected scFv to full length human IgG1 vestors using a PCR-amplification wherein primers used, are:

primers for amplification of VH-segments:
5'VH: 5'-GGT*GTGCATTC*CGAGGTGCAGCTGTTGGAG (SEQ. ID. NO: 13)
3'VH: 5'-GA*CGTACG***ACTCACCT**GAGCTCACGGTGACCAG (SEQ. ID. NO: 14)

and primers for amplification of VL-segments:
5'VL: 5'-GGT*GTGCATTC*CCAGTCTGTGCTGACTCAG (SEQ. ID. NO: 15)
3'VL: 5'-GA*CGTACG*TTCTACTCACCTAGGACCGTCAGCTT (SEQ. ID. NO: 16)

13. Method according to claim 12, wherein colonies containing heavy chain regions and light chain region plasmids with variable heavy region and variable light chain inserts were identified by colony PCR using

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Forward primer: 5'-ATGGGTGACAATGACATC (SEQ. ID. NO: 17)
Reverse primer: 5'-AAGCTTGCTAGCGTACG (SEQ. ID. NO: 18)

14. Method for passive immunzation of mammals, preferably humans, wherein a therapeutically or prophylactically effective amount of a recombinant human antibody directed towards at least one oxidized fragment of apolipoprotein B is administered for treatment of atherosclerosis.

15. Method according to claim 14, the oxidized fragment is selected from one or more of the group consisting of
FLDTVYGNCSTHFTVKTRKG
PQCSTHILQWLKRVHANPLL
VISIPRLQAEARSEILAHWS
KLVKEALKESQLPTVMDFRK
LKFVTQAEGAKQTEATMTFK
DGSLRHKFLDSNIKFSHVEK
KGTYGLSCQRDPNTGRLNGE
RLNGESNLRFNSSYLQGTNQ
SLTSTSDLQSGIIKNTASLK
TASLKYENYELTLKSDTNGK
DMTFSKQNALLRSEYQADYE
MKVKIIRTIDQMQNSELQWP
IALDDAKINFNEKLSQLQTY
KTTKQSFDLSVKAQYKKNKH
EEEMLENVSLVCPKDATRFK
GSTSHHLVSRKSISAALEHK
IENIDFNKSGSSTASWIQNV
IREVTQRLNGEIQALELPQK
EVDVLTKYSQPEDSLIPFFE
HTFLIYITELLKKLQSTTVM
LLDIANYLMEQIQDDCTGDE
CTGDEDYTYKIKRVIGNMGQ
GNMGQTMEQLTPELKSSILK
SSILKCVQSTKPSLMIQKAA
IQKAAIQALRKMEPKDKDQE
RLNGESNLRFNSSYLQGTNQ
SLNSHGLELNADILGTDKIN
WIQNVDTKYQIRIQIQEKLQ
TYISDWWTLAAKNLTDFAEQ

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EATLQRIYSLWEHSTKNHLQ
ALLVPPETEEAKQVLFLDTV
IEIGLEGKGFEPTLEALFGK
SGASMKLTTNGRFREHNAKF
NLIGDFEVAEKINAFRAKVH
GHSVLTAKGMALFGEGKAEF
FKSSVITLNTNAELFNQSDI
FPDLGQEVALNANTKNQKIR,
or an active site thereof.

16. Method according to claims 14-15, wherein the antibody is characterized in that it comprises
the variable heavy region(V_H)

gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcac
cttcaataacgcctggatgagctgggtccgccaggctccagggaaggggctggagtgggtctcatccattagtagtagtagt
agttacatatactacgcagactcagtgaagggccgattcaccatctccagagacaattccaagaacacgctgtatctgcaaat
gaacagcctgagagccgaggacactgccgtgtattactgtgcgagagtcagtaggtactactacggaccatctttctactttga
ctcctggggccagggtacactggtcaccgtgagcagc

and the variable light region (V_L)

cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgctctggaagcaggtccaa
cattgggaataattatgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctatggtaacaacaatcggcc
ctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatga
ggctgattattactgtgcagcatgggatgacagcctgaatggtcattgggtgttcggcggaggaaccaagctgacggtccta
ggt.

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17. Method according to claims 14-15, wherein the antibody is characterized in that it comprises
the variable heavy region (V_H)

gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcggcctctggattcac
cttcagtgactactacatgagctgggtccgccaggctcccgggaaggggctggagtgggtatcgggtgttagttggaatggc
agtaggacgcactatgcagactctgtgaagggccgattcaccatctccagagacaattccaagaacacgctgtatctgcaaat
gaacagcctgagagccgaggacactgccgtgtattactgtgcgagagcggctaggtactcctactactactacggtatggac
gtctggggccaaggtacactggtcaccgtgagcagc

and the variable light region (V_L)

cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgttctggaagcagctccaa
catcggaaataatgctgtaaactggtatcagcagctcccaggaacggcccccaaactcctcatctatgggaatgatcggcgg
ccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggat
gaggctgattattactgtcagacctggggcactggccgggggtattcggcggaggaaccaagctgacggtcctaggt

18. Method according to claims 14-15, wherein the antibody is characterized in that it comprises
the variable heavy region (V_H)

gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcac
ctttagtagctattggatgagctgggtccgccaggctccagggaaggggctggagtgggtctcaagtatcagtggtagtggtc
gtaggacatactacgcagactccgtgcagggccggttcaccatctccagagacaattccaagaacacgctgtatctgcaaatg
aacagcctgagagccgaggacactgccgtgtattactgtgcgagattggtctcctatggttcggggagtttcggttttgactact
ggggccaaggtacactggtcaccgtgagcagc

and the variable light region (V_L)

cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaat
atcggaagtaattatgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctatggtaactacaatcggccc
tcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatgag
gctgattattactgtgcagcatgggatgacagcctgagtggttgggtgttcggcggaggaaccaagctgacggtcctaggt

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19. Method according to claims 14-15, wherein the antibody is characterized in that it comprises the variable heavy region (V_H)

gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcac
cttcagtaacgcctggatgagctgggtccgccaggttccagggaaggggctggagtgggtctcaactcttggtggtagtggt
ggtggtagcacatactacgcagactccgtgaagggccggttcaccatctccagagacaattccaagaacacgctgtatctgc
aaatgaacagcctgagagccgaggacactgccgtgtattactgtgcgaagttagggggcgatcccgatatgggcggtggc
cccgccaatttgactactggggccaaggtacactggtcaccgtgagcagc

and the variable light region (V_L)

cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgctctggaagcagctccaa
cattggaaataactatgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggcc
ctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatga
ggctgattattactgtgcagcatgggatgacagcctgagtcattggctgttcggcggaggaaccaagctgacggtcctaggt

20. Method according to claims 14-15, wherein the antibody is characterized in that it comprises the variable heavy region (V_H)

gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcac
cttcagtgactactacatgagctggatccgccaggctccagggaaggggctggagtgggtctcaagtatcagtggccgtggg
ggtagttcctactacgcagactccgtgaggggccggttcaccatctccagagacaattccaagaacacgctgtatctgcaaat
gaacagcctgagagccgaggacactgccgtgtattactgtgcgagactttcctacagctatggttacgagggggcctactact
ttgactactggggccagggtacactggtcaccgtgagcagc

and the variable light region (V_L)

cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgctctggaagcagctccaa
cattgggaataattatgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctataggaataatcagcggcc
ctcaggggtccctgaccgattctctggctccaagtctggcaccttagcctccctggccatcagtgggctccggtccgaggatga
ggctgattattactgtgcaacctgggatgacagcctgaatggttgggtgttcggcggaggaaccaagctgacggtcctaggt

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21. Method according to claims 14-15, wherein the antibody is characterized in that it comprises
the variable heavy region (V_H)

gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcac
ctttagcagctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcatccattagtagtagtggtc
gtttcatttactacgcagactcaatgaagggccgcttcaccatctccagagacaattccaagaacacgctgtatctgcaaatga
acagcctgagagccgaggacactgccgtgtattactgtacgaggctccggagagggagctacttctgggcttttgatatctgg
ggccaaggtacactggtcaccgtgagcagc

and the variable light region (V_L)

cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgttctggaagcagctccaa
cattggcggtgagtctgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggcc
ctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatga
ggctgattattactgtgcagcatgggatgacagcctgaatggttgggtgttcggcggaggaaccaagctgacggtcctaggt

22. Pharmaceutical composition comprising a recombinant human antibody directed towards at least one oxidized fragment of apolipoprotein B for therapeutical or prophylactical treatment of atherosclerosis by means of passive immunization.

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ABSTRACT

The present invention relates to passive immunization for treating or preventing atherosclerosis using a a recombinant human antibody directed towards at least one oxidized fragment of apolipoprotein B in the manufacture of a pharmaceutical composition for therapeutical or prophylactical treatment of atherosclerosis by means of passive immunization, as well as method for preparing such antibodies, and a method for treating a mammal, preferably a human using such an antibody to provide for passive immunization.

(FIG. 1A)

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FIG. 1

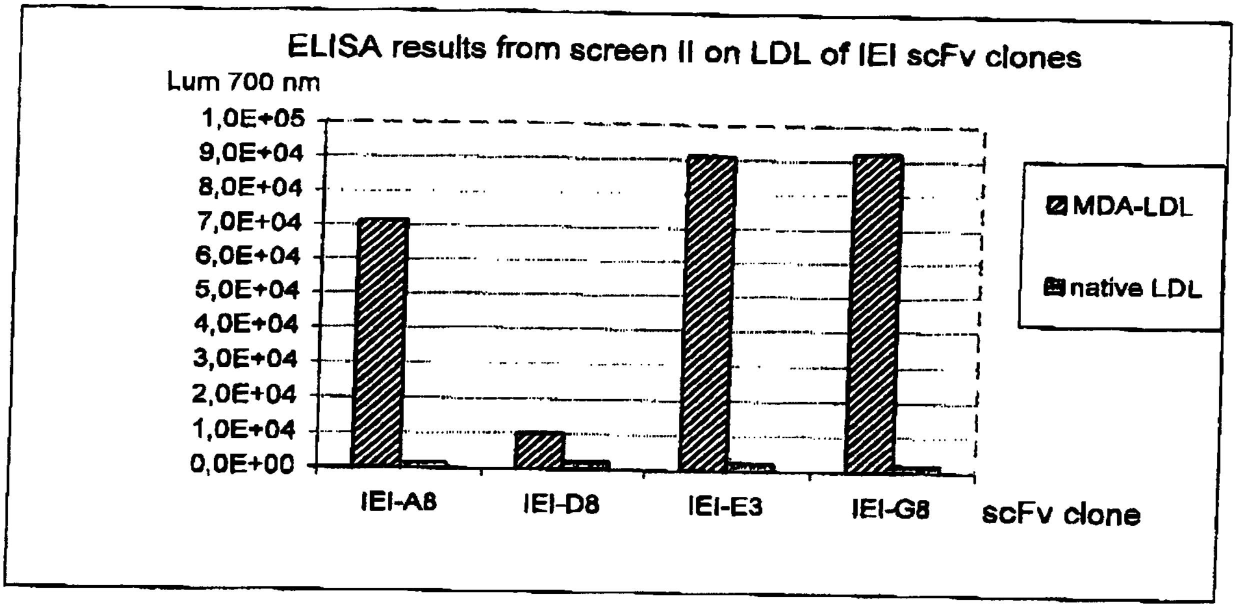

FIG. 1A

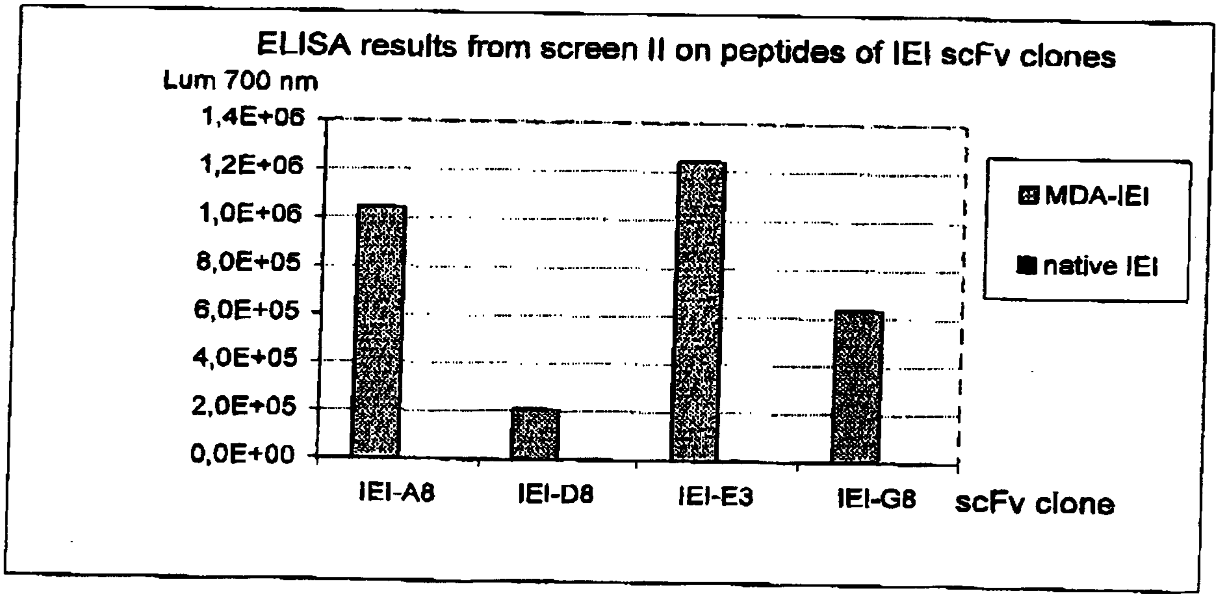

FIG. 1B

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FIG. 1 cont'd

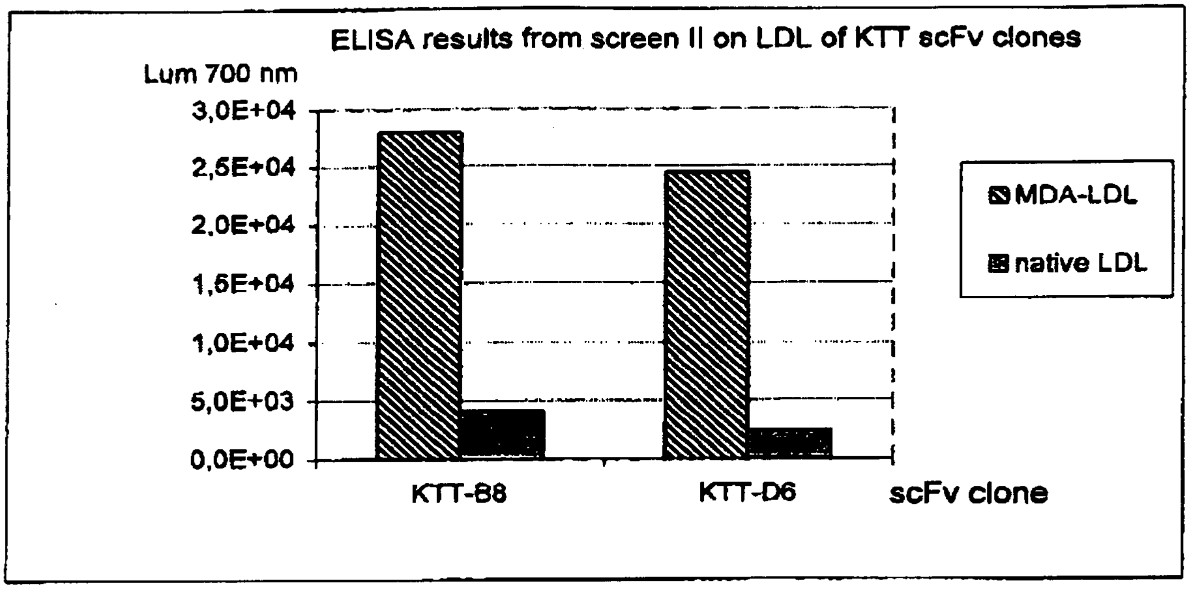

FIG. 1C

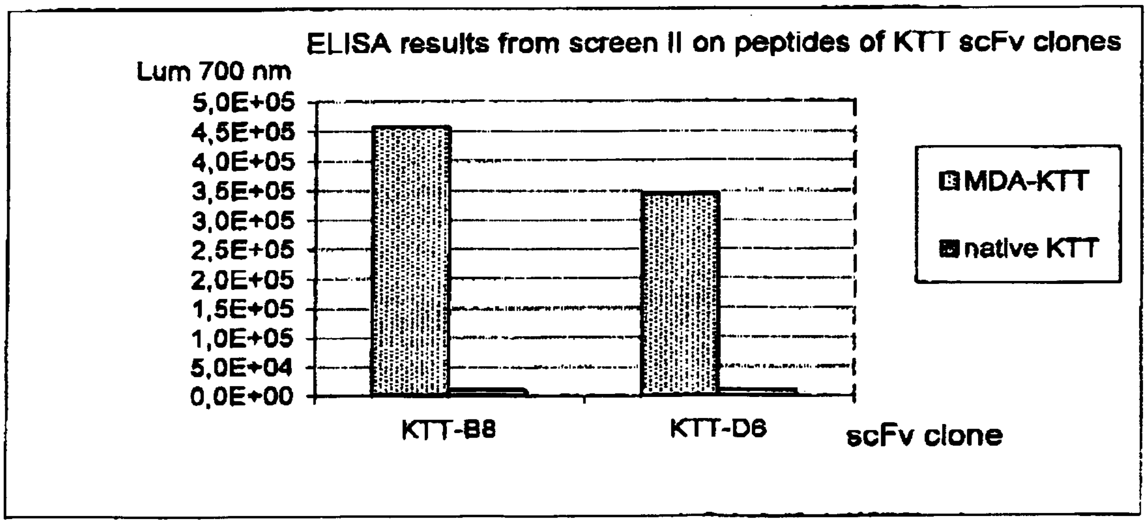

FIG. 1D

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FIG. 2

Results from screening III titration of scFv on MDA modified LDL and non-modified native LDL

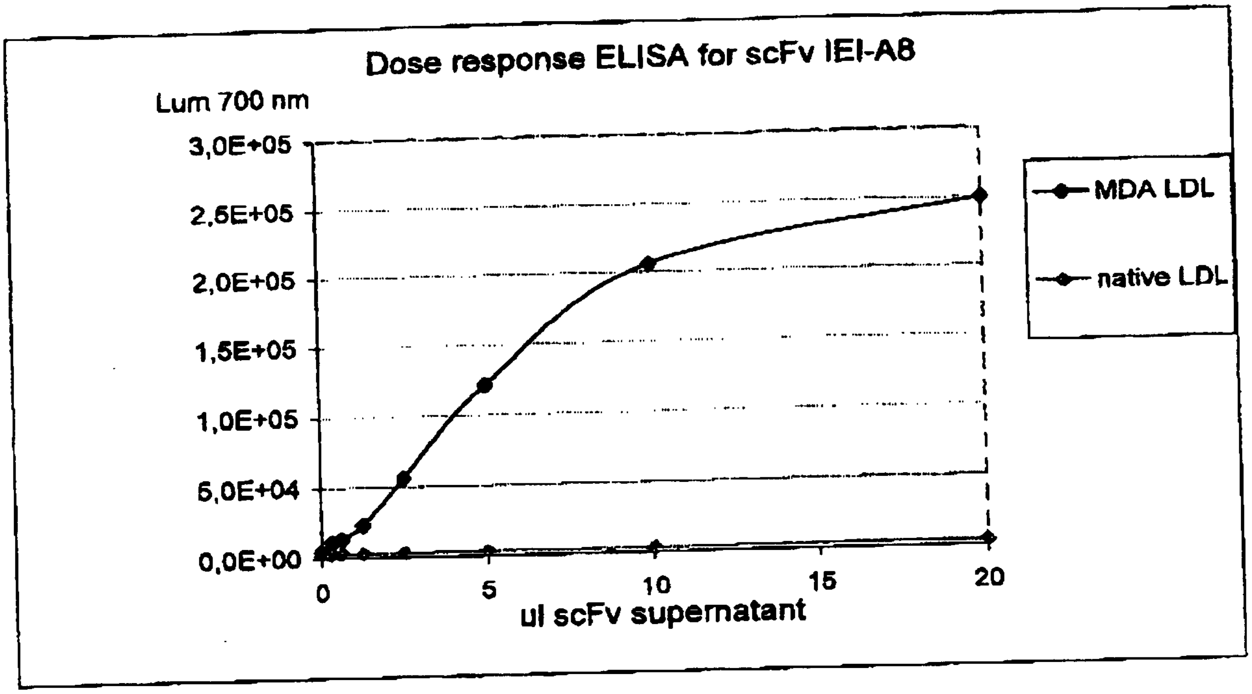

FIG. 2A

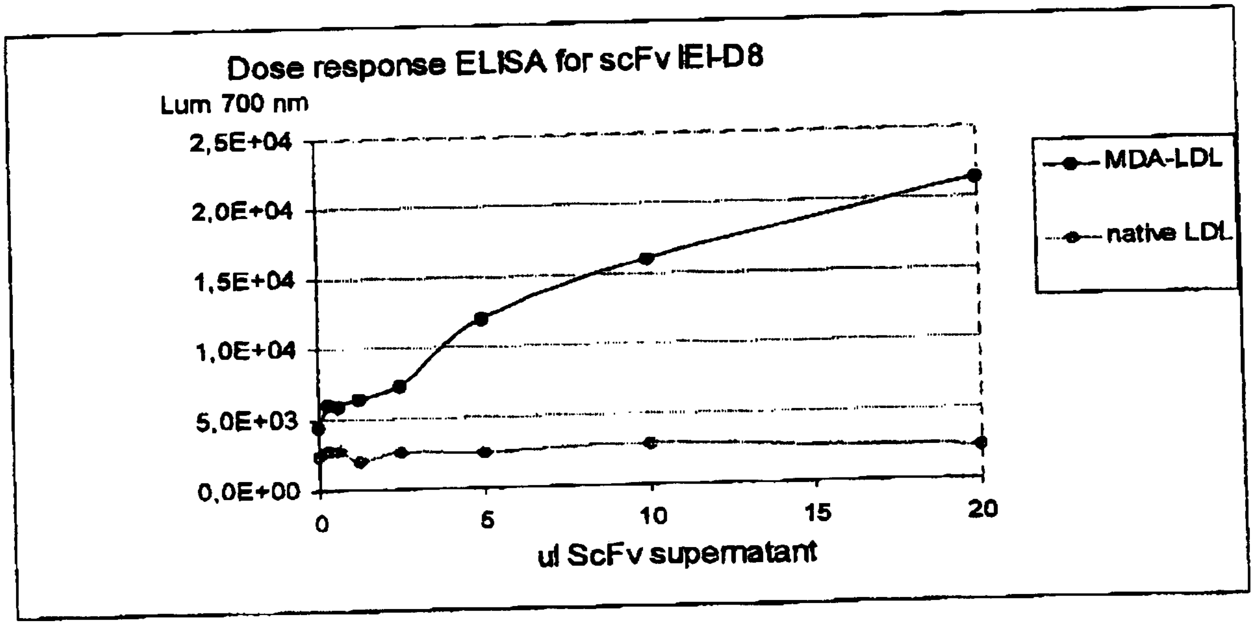

FIG. 2B

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FIG. 2 cont'd

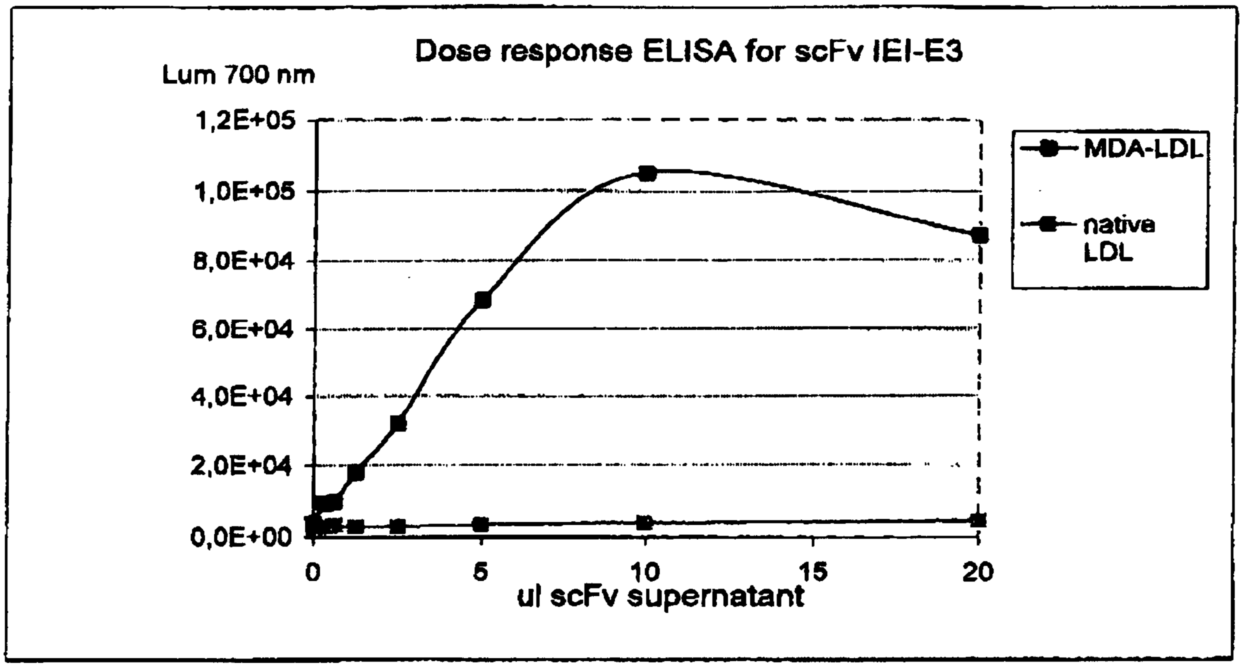

FIG. 2C

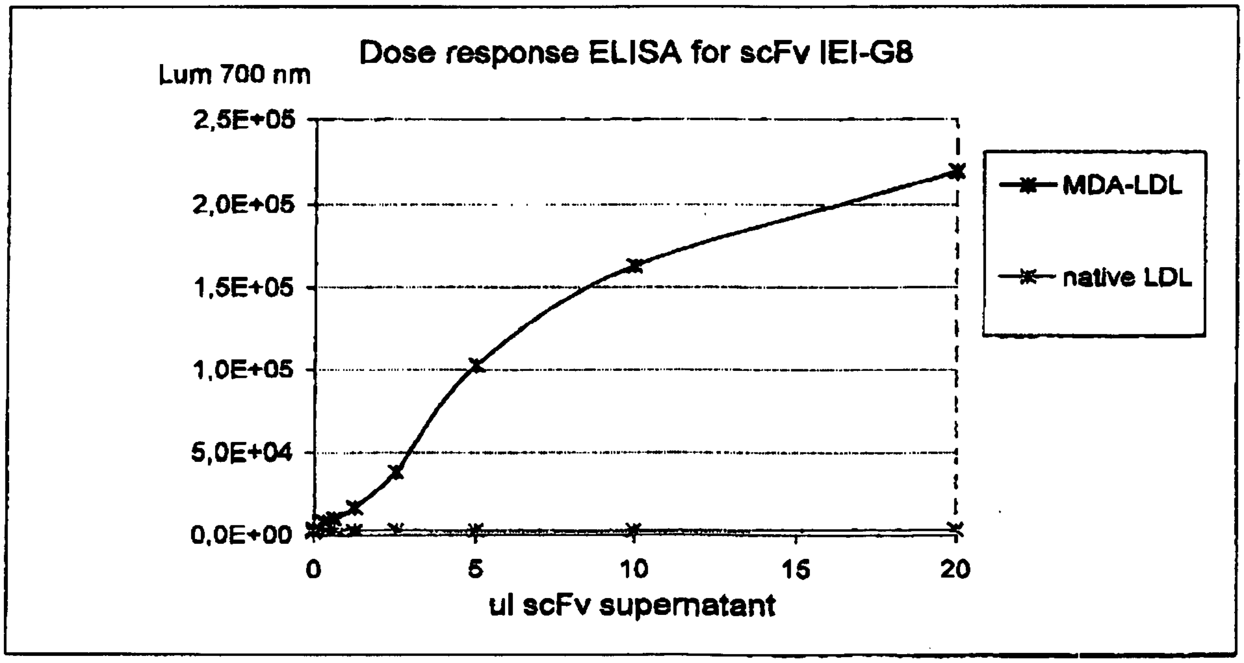

FIG. 2D

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FIG. 2 cont'd

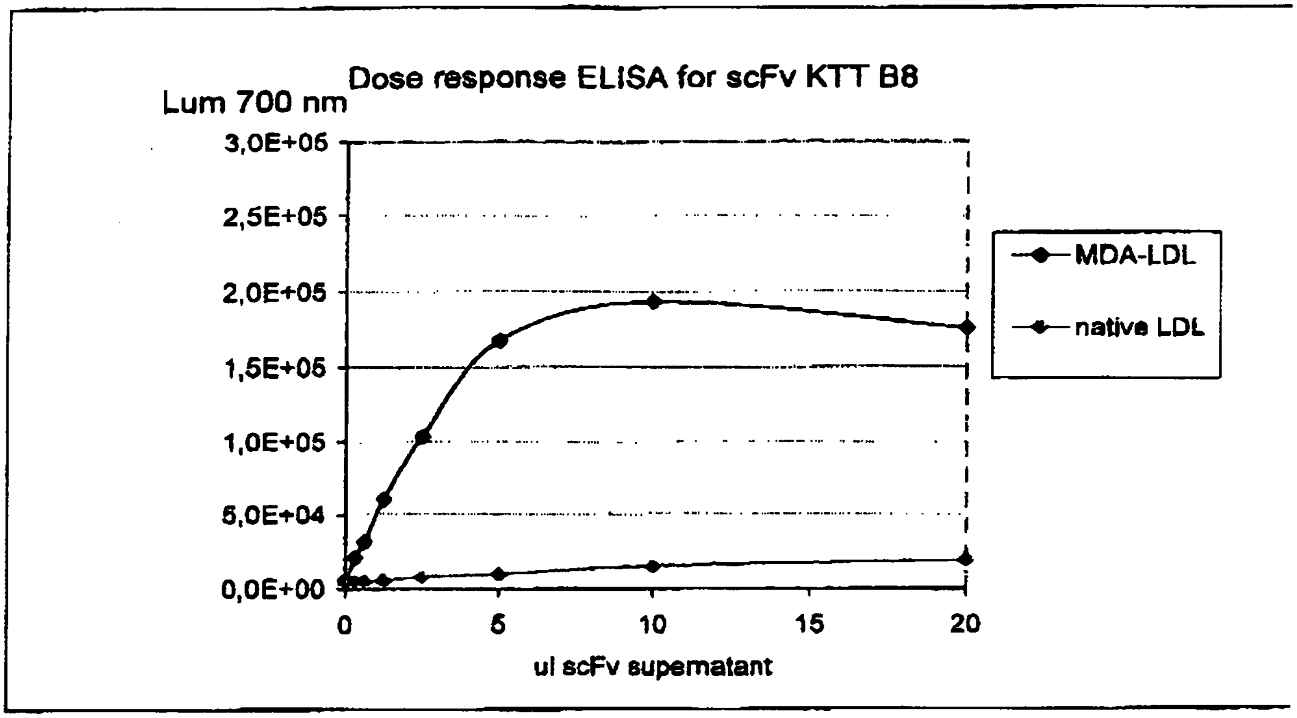

FIG. 2E

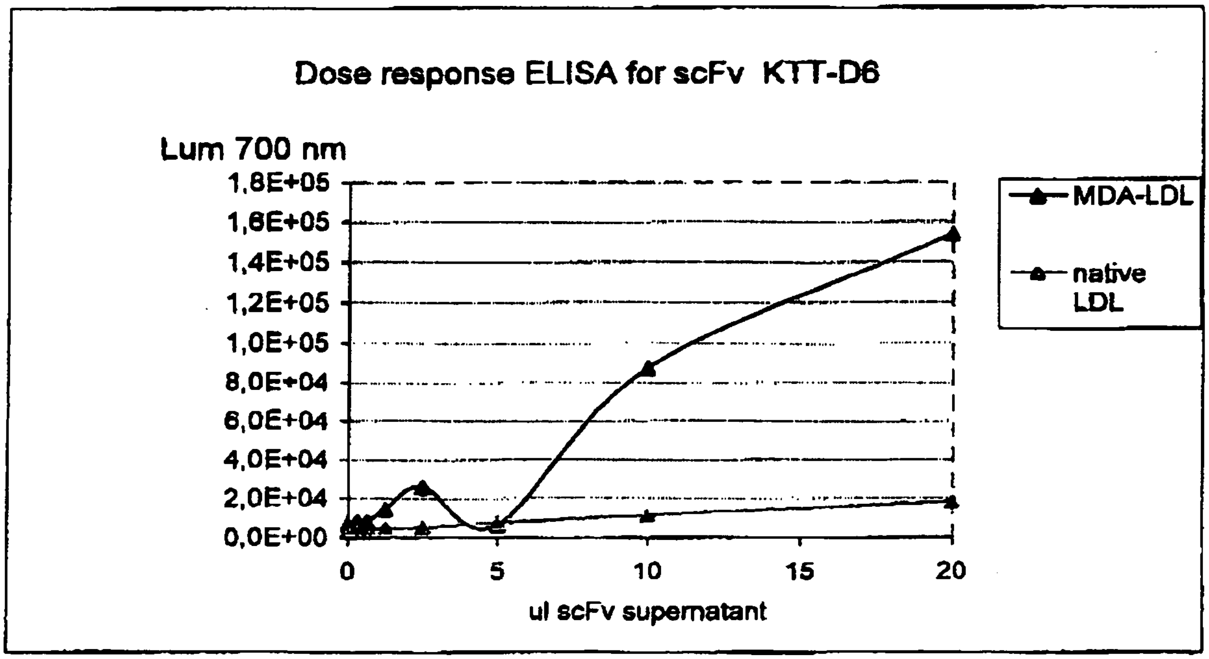

FIG. 2F

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FIG. 3

DNA sequences of the variable regions in the six scFv that bind MDA modified ApoB-100 peptides.

IEIA8

Variable heavy region (V_H)

gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcac
cttcaataacgcctggatgagctgggtccgccaggctccagggaaggggctggagtgggtctcatccattagtagtagtagt
agttacatatactacgcagactcagtgaagggccgattcaccatctccagagacaattccaagaacacgctgtatctgcaaat
gaacagcctgagagccgaggacactgccgtgtattactgtgcgagagtcagtaggtactactacggaccatctttctactttga
ctcctggggccagggtacactggtcaccgtgagcagc

Variable light region (V_L)

cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgctctggaagcaggtccaa
cattgggaataattatgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctatggtaacaacaatcggcc
ctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatga
ggctgattattactgtgcagcatgggatgacagcctgaatggtcattgggtgttcggcggaggaaccaagctgacggtccta
ggt

IEI-E3

Variable heavy region (V_H)

gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcggcctctggattcac
cttcagtgactactacatgagctgggtccgccaggctcccgggaaggggctggagtgggtatcgggtgttagttggaatggc
agtaggacgcactatgcagactctgtgaagggccgattcaccatctccagagacaattccaagaacacgctgtatctgcaaat
gaacagcctgagagccgaggacactgccgtgtattactgtgcgagagcggctaggtactcctactactactacggtatggac
gtctggggccaaggtacactggtcaccgtgagcagc

Variable light region (V_L)

cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgttctggaagcagctccaa
catcggaaataatgctgtaaactggtatcagcagctcccaggaacggcccccaaactcctcatctatgggaatgatcggcgg
ccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggat
gaggctgattattactgtcagacctggggcactggccgggggtattcggcggaggaaccaagctgacggtcctaggt

IEI-G8

Variable heavy region (V_H)

gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcac
ctttagtagctattggatgagctgggtccgccaggctccagggaaggggctggagtgggtctcaagtatcagtggtagtggtc
gtaggacatactacgcagactccgtgcagggccggttcaccatctccagagacaattccaagaacacgctgtatctgcaaatg
aacagcctgagagccgaggacactgccgtgtattactgtgcgagattggtctcctatggttcggggagtttcggttttgactact
ggggccaaggtacactggtcaccgtgagcagc

Variable light region (V_L)

cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcttgttctggaagcagctccaat
atcggaagtaattatgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctatggtaactacaatcggccc
tcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatgag
gctgattattactgtgcagcatgggatgacagcctgagtggttgggtgttcggcggaggaaccaagctgacggtcctaggt

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IEI-D8

Variable heavy region (V_H)
gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcaccttcagtaacgcctggatgagctgggtccgccaggttccagggaaggggctggagtgggtctcaactcttggtggtagtggtggtggtagcacatactacgcagactccgtgaagggccggttcaccatctccagagacaattccaagaacacgctgtatctgcaaatgaacagcctgagagccgaggacactgccgtgtattactgtgcgaagttagggggcgatcccgatatgggcggtggccccgccaatttgactactggggccaaggtacactggtcaccgtgagcagc

Variable light region (V_L)
cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgctctggaagcagctccaacattggaaataactatgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatgaggctgattattactgtgcagcatgggatgacagcctgagtcattggctgttcggcggaggaaccaagctgacggtcctaggt

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Variable heavy region (V_H)
gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcaccttcagtgactactacatgagctggatccgccaggctccagggaaggggctggagtgggtctcaagtatcagtggccgtggggtagttcctactacgcagactccgtgaggggccggttcaccatctccagagacaattccaagaacacgctgtatctgcaaatgaacagcctgagagccgaggacactgccgtgtattactgtgcgagactttcctacagctatggttacgagggggcctactacttgactactggggccagggtacactggtcaccgtgagcagc

Variable light region (V_L)
Cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgctctggaagcagctccaacattgggaataattatgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctataggaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcaccttagcctccctggccatcagtgggctccggtccgaggatgaggctgattattactgtgcaacctgggatgacagcctgaatggttgggtgttcggcggaggaaccaagctgacggtcctaggt

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Variable heavy region (V_H)
gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctctggattcacctttagcagctatgccatgagctgggtccgccaggctccagggaaggggctggagtgggtctcatccattagtagtagtggtcgtttcatttactacgcagactcaatgaagggccgcttcaccatctccagagacaattccaagaacacgctgtatctgcaaatgaacagcctgagagccgaggacactgccgtgtattactgtacgaggctccggagagggagctacttctgggcttttgatatctggggccaaggtacactggtcaccgtgagcagc

Variable light region (V_L)
cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgttctggaagcagctccaacattggcggtgagtctgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctatagtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgaggatgaggctgattattactgtgcagcatgggatgacagcctgaatggttgggtgttcggcggaggaaccaagctgacggtcctaggt

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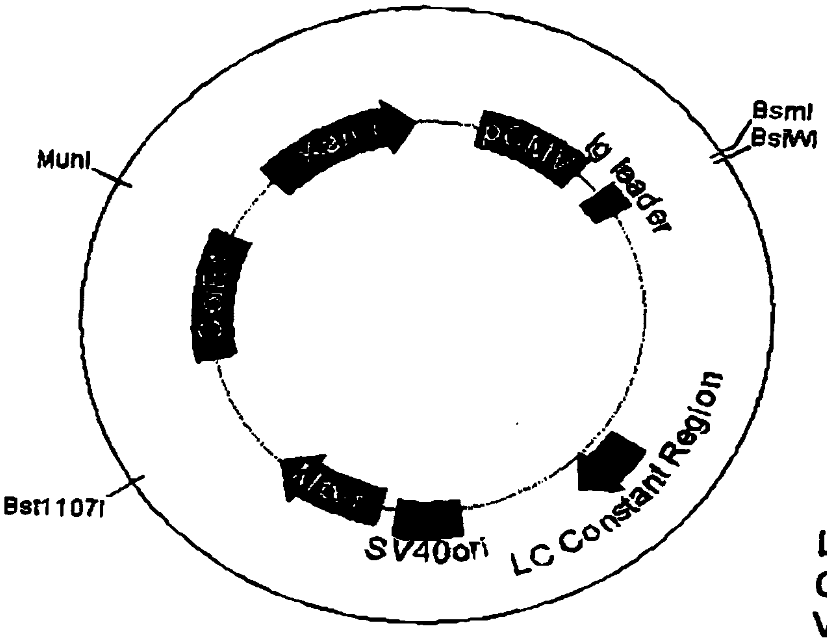
FIG. 4



Light
Chain
Vector

FIG. 4A

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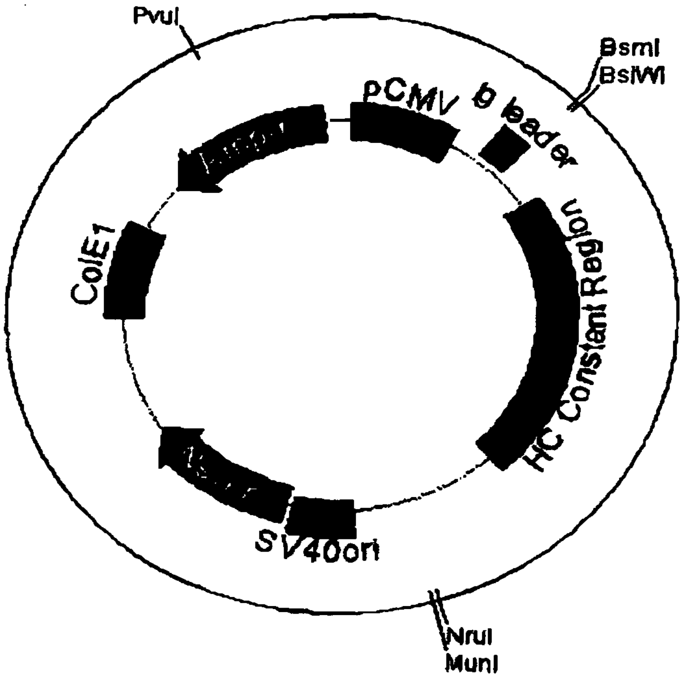
FIG. 4 cont'd



Heavy Chain vector

FIG. 4B

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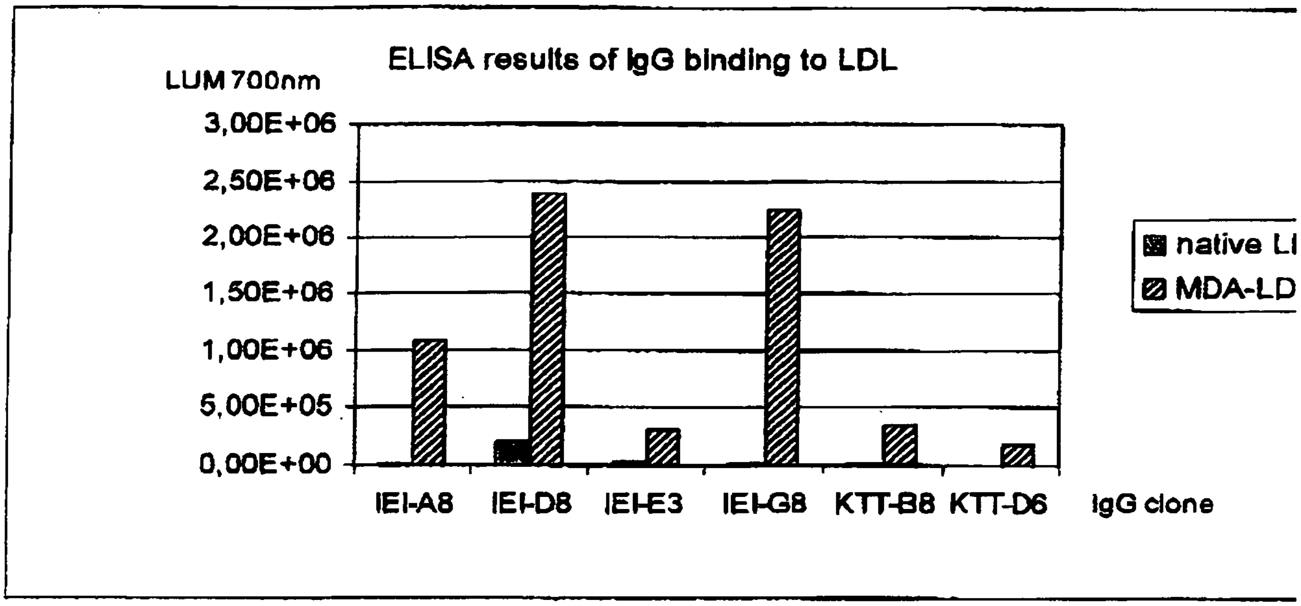
FIG. 5



This graph shows the result from 25 ng purified IgG detected with rabbit-anti-Human IgG-HRP (DAKO P214) and luminescence at 700nm. The plate was coated with 0.5 µg LDL/well.

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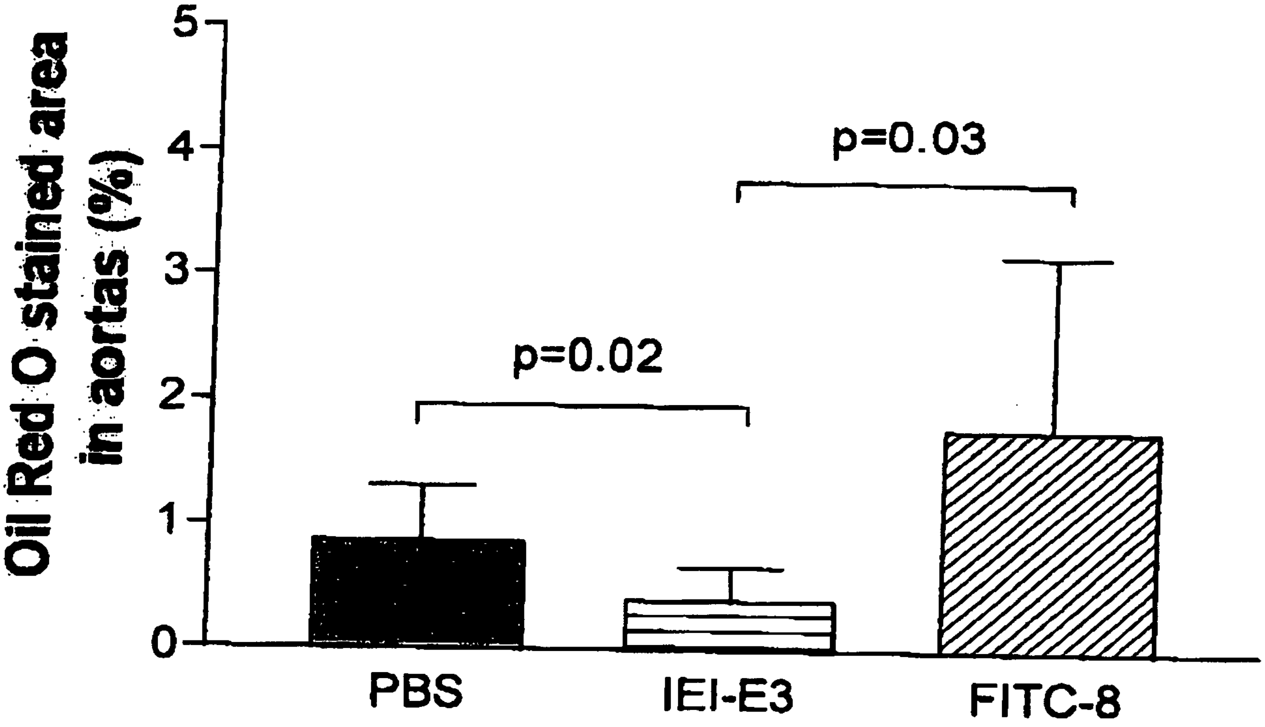

FIG. 6

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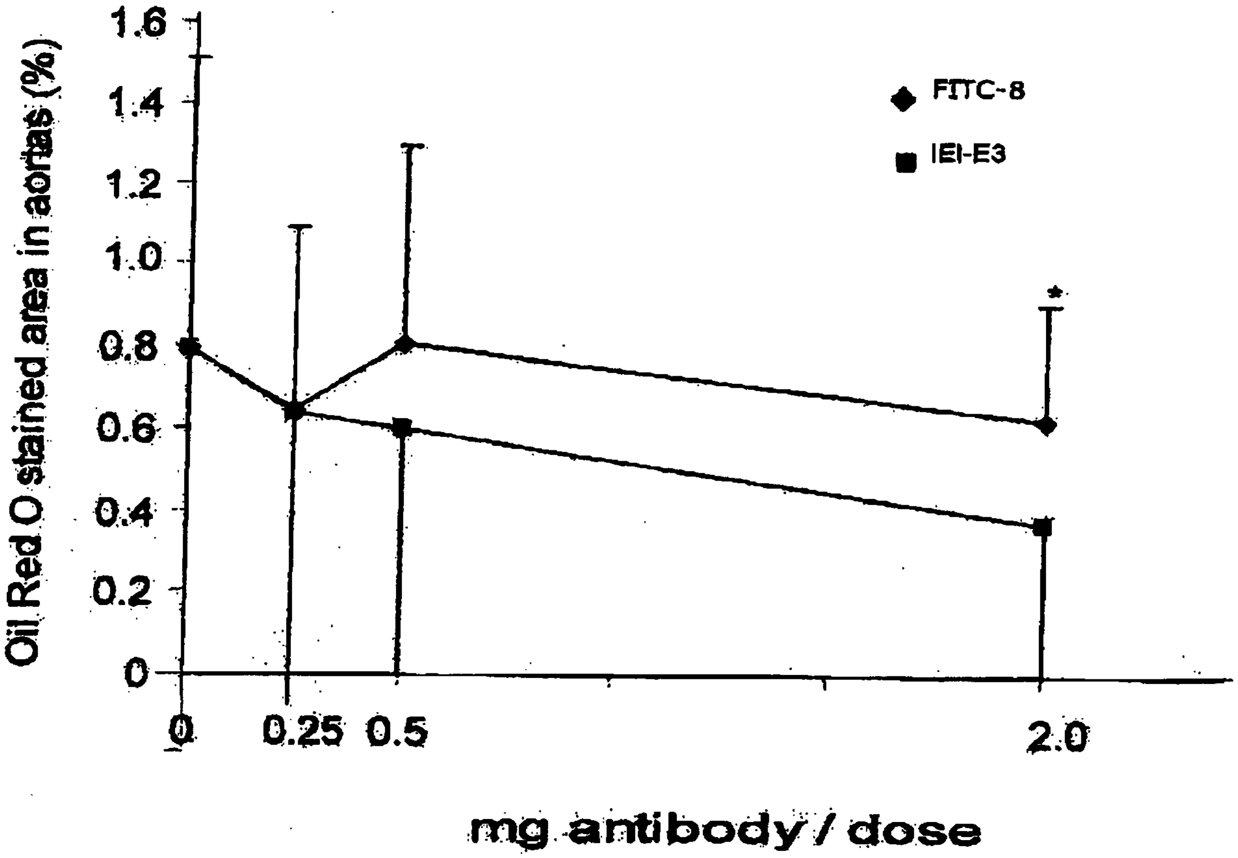

FIG. 7

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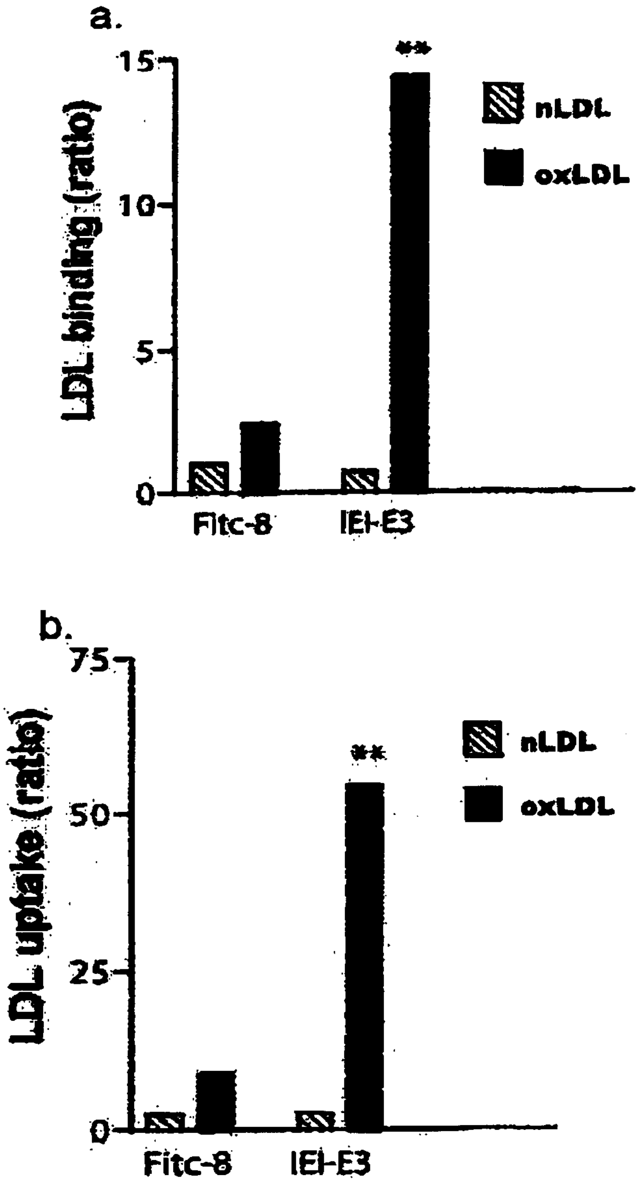

FIG. 8

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SEQ. ID. NO: 1

IEIA8

Variable heavy region (V_H)
gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctct
ggattcaccttcaataacgcctggatgagctgggtccgccaggctccagggaaggggctggagtgggtctcatcc
attagtagtagtagtagttacatatactacgcagactcagtgaagggccgattcaccatctccagagacaattcc
aagaacacgctgtatctgcaaatgaacagcctgagagccgaggacactgccgtgtattactgtgcgagagtcagt
aggtactactacggaccatctttctactttgactcctggggccagggtacactggtcaccgtgagcagc

SEQ. ID. NO: 2

IEIA8

Variable light region (V_L)
cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgctctggaagc
aggtccaacattgggaataattatgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctat
ggtaacaacaatcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggcc
atcagtgggctccggtccgaggatgaggctgattattactgtgcagcatgggatgacagcctgaatggtcattgg
gtgttcggcggaggaaccaagctgacggtcctaggt

SEQ. ID. NO: 3

IEI-E3

Variable heavy region (V_H)
gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcggcctct
ggattcaccttcagtgactactacatgagctgggtccgccaggctcccgggaaggggctggagtgggtatcgggt
gttagttggaatggcagtaggacgcactatgcagactctgtgaagggccgattcaccatctccagagacaattcc
aagaacacgctgtatctgcaaatgaacagcctgagagccgaggacactgccgtgtattactgtgcgagagcggct
aggtactcctactactactacggtatggacgtctggggccaaggtacactggtcaccgtgagcagc

SEQ. ID. NO: 4

IEI-E3

Variable light region (V_L)
cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgttctggaagc
agctccaacatcggaaataatgctgtaaactggtatcagcagctcccaggaacggcccccaaactcctcatctat
gggaatgatcggcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggcc
atcagtgggctccggtccgaggatgaggctgattattactgtcagacctggggcactggccgggggtattcggc
ggaggaaccaagctgacggtcctaggt

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SEQ. ID. NO: 5

IEI-G8

Variable heavy region (V_H)

gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctc
ctgtgcagcctctggattcacctttagtagctattggatgagctgggtccgccaggctccag
ggaaggggctggagtgggtctcaagtatcagtggtagtggtcgtaggacatactacgcagac
tccgtgcagggccggttcaccatctccagagacaattccaagaacacgctgtatctgcaaat
gaacagcctgagagccgaggacactgccgtgtattactgtgcgagattggtctcctatggtt
cggggagtttcggttttgactactggggccaaggtacactggtcaccgtgagcagc

SEQ. ID. NO: 6

IEI-G8

Variable light region (V_L)

cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctc
ttgttctggaagcagctccaatatcggaagtaattatgtatcctggtatcagcagctcccag
gaacggcccccaaactcctcatctatggtaactacaatcggccctcaggggtccctgaccga
ttctctggctccaagtctggcacctcagcctccctggccatcagtgggctccggtccgagga
tgaggctgattattactgtgcagcatgggatgacagcctgagtggttgggtgttcggcggag
gaaccaagctgacggtcctaggt

SEQ. ID. NO: 7

IEI-D8

Variable heavy region (V_H)

gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcagcctct
ggattcaccttcagtaacgcctggatgagctgggtccgccaggttccagggaaggggctggagtgggtctcaact
cttggtggtagtggtggtggtagcacatactacgcagactccgtgaagggccggttcaccatctccagagacaat
tccaagaacacgctgtatctgcaaatgaacagcctgagagccgaggacactgccgtgtattactgtgcgaagtta
ggggggcgatcccgatatgggcggtggccccgccaatttgactactggggccaaggtacactggtcaccgtgagc
agc

SEQ. ID. NO: 8

IEI-D8

Variable light region (V_L)

cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgctctggaagc
agctccaacattggaaataactatgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctat
agtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggcc
atcagtgggctccggtccgaggatgaggctgattattactgtgcagcatgggatgacagcctgagtcattggctg
ttcggcggaggaaccaagctgacggtcctaggt

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SEQ. ID. NO: 9

KTT-D6

Variable heavy region (V_H)
gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctc
ctgtgcagcctctggattcaccttcagtgactactacatgagctggatccgccaggctccag
ggaaggggctggagtgggtctcaagtatcagtggccgtgggggtagttcctactacgcagac
tccgtgaggggccggttcaccatctccagagacaattccaagaacacgctgtatctgcaaat
gaacagcctgagagccgaggacactgccgtgtattactgtgcgagactttcctacagctatg
gttacgaggggggcctactactttgactactggggccagggtacactggtcaccgtgagcagc

SEQ. ID. NO: 10

KTT-D6

Variable light region (V_L)
cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgctctggaagc
agctccaacattgggaataattatgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctat
aggaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcaccttagcctccctggcc
atcagtgggctccggtccgaggatgaggctgattattactgtgcaacctgggatgacagcctgaatggttgggtg
ttcggcggaggaaccaagctgacggtcctaggt

SEQ. ID. NO: 11

KTT-B8

Variable heavy region (V_H)
gaggtgcagctgttggagtctgggggaggcttggtacagcctggggggtccctgagactctc
ctgtgcagcctctggattcacctttagcagctatgccatgagctgggtccgccaggctccag
ggaaggggctggagtgggtctcatccattagtagtagtggtcgtttcatttactacgcagac
tcaatgaagggccgcttcaccatctccagagacaattccaagaacacgctgtatctgcaaat
gaacagcctgagagccgaggacactgccgtgtattactgtacgaggctccggagagggagct
acttctgggcttttgatatctggggccaaggtacactggtcaccgtgagcagc

SEQ. ID. NO: 12

KTT-B8

Variable light region (V_L)
cagtctgtgctgactcagccaccctcagcgtctgggacccccgggcagagggtcaccatctcctgttctggaagc
agctccaacattggcggtgagtctgtatcctggtatcagcagctcccaggaacggcccccaaactcctcatctat
agtaataatcagcggccctcaggggtccctgaccgattctctggctccaagtctggcacctcagcctccctggcc
atcagtgggctccggtccgaggatgaggctgattattactgtgcagcatgggatgacagcctgaatggttgggtg
ttcggcggaggaaccaagctgacggtcctaggt

SEQ. ID. NO: 13

5'VH: 5'-GGT*GTGCATTCC*GAGGTGCAGCTGTTGGAG

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SEQ. ID. NO: 14

3'VH: 5'-GA*CGTACG***ACTCACCT**GAGCTCACGGTGACCAG

SEQ. ID. NO: 15

5'VL: 5'-GGT*GTGCATTC*CCAGTCTGTGCTGACTCAG

SEQ. ID. NO: 16

3'VL: 5'-GA*CGTACG*TTCT**ACTCACCT**AGGACCGTCAGCTT

SEQ. ID. NO: 17

5'-ATGGGTGACAATGACATC

SEQ. ID. NO: 18

5'-AAGCTTGCTAGCGTACG